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RESULT 1	ID	AA083841	standard; Protein; 212 AA
XX	XX	AA083841;	
XX	DT	08-MAY-2002	(first entry)
DE	XX	Bacillus lipase polypeptide #1.	
KW	KW	Lipase; Bacillus; animal feed; flava	
KW	KW	human foodstuff; cheese; food emulsi	
KW	KW	leather processing; cleaning agent;	
KW	KW	cellulose disease; indigestion; obes	
KW	KW	gastrointestinal lipid related conom	
XX	XX	gastrointestinal.	
OS	XX	Bacillus pumilus.	
XX	XX	WO200206457-A2.	
XX	PD	24-JAN-2002.	
XX	PE	13-JUL-2001; 2001WO-US22160.	
XX	XX	13-JUL-2000; 2000US-217954P.	
XX	PR	21-JUN-2001; 2001US-300378P.	
PA	XX	(MAXY-) MAXYGEN INC.	
PI	XX	Givier LJ, Minshall J, Vogel K;	
XX	OR	WPI; 2002-171805/22.	

DR N-PSDB; ABR33819.
XX Nucleic acids encoding lipase enzymes which are useful as supplements
PT in animal feeds, as agents of flavour modification and for treating
PT Crohn's disease and coeliac disease -
XX
PS Claim 20; Page 138; 196pp; English.
XX
CC The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AA083841-AA083897 represent Bacillus lipase
CC polypeptides of the invention.
XX
SQ Sequence 212 AA;
Query Match 100.0%; Score 1088; DB 23; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.6e-103;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKFVKRRILAVTLVSVTSFLFAMOPSAKAEHNPPVVMHVGIGASYNFAGIKSYLVQ 60
DB 1 MKFVKRRILAVTLVSVTSFLFAMOPSAKAEHNPPVVMHVGIGASYNFAGIKSYLVQ 60
QY 61 GWSRGKLYAVDFMDKGTGNTNNGPVLSEFYQKVLDEFGAKKVDIVAHSMGANTPYITKN 120
DB 61 GWSRGKLYAVDFMDKGTGNTNNGPVLSEFYQKVLDEFGAKKVDIVAHSMGANTPYITKN 120
QY 121 LDGNGKIEENVYTLGAGNSTSKALPGTDPNOKILYISYSSADMIYNNYLSKIDGAKNA 180
DB 121 LDGNGKIEENVYTLGAGNSTSKALPGTDPNOKILYISYSSADMIYNNYLSKIDGAKNA 180
QY 181 QIHGVGHIGILMNSQVNSLIKEGLNGGQNTN 212
DB 181 QIHGVGHIGILMNSQVNSLIKEGLNGGQNTN 212
RESULT 2
AA083847
ID AA083847 standard; Protein: 212 AA.
AC AA083847;
XX
DT 08-MAY-2002 (first entry)
XX
DE Bacillus lipase polypeptide #7.
XX
KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
KW gastrointestinal.
XX
OS Bacillus firmus.
XX
PN WO200206457-A2.
XX
PD 24-JAN-2002.
XX
PF 13-JUL-2001; 2001WO-US22160.
XX
PR 13-JUL-2000; 2000US-217954P.
XX
PR 21-JUN-2001; 2001US-300378P.
XX

PA (MAXY-) MAXYGEN INC.
XX
PI Glycer LJ, Minshull J, Vogel K;
XX
DR WPI: 2002-171805/22.
XX
DR N-PSDB; ABR33825.
XX
PT Nucleic acids encoding lipase enzymes which are useful as supplements
PT in animal feeds, as agents of flavour modification and for treating
PT Crohn's disease and coeliac disease -
XX
PS Claim 20; Page 139; 196pp; English.
XX
CC The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AA083841-AA083897 represent Bacillus lipase
CC polypeptides of the invention.
XX
SQ Sequence 212 AA;
Query Match 98.1%; Score 1067; DB 23; Length 212;
Best Local Similarity 98.6%; Pred. No. 2.3e-101;
Matches 209; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MKFVKRRILAVTLVSVTSFLFAMOPSAKAEHNPPVVMHVGIGASYNFAGIKSYLVQ 60
DB 1 MKFVKRRILAVTLVSVTSFLFAMOPSAKAEHNPPVVMHVGIGASYNFAGIKSYLVQ 60
QY 61 GWSRGKLYAVDFMDKGTGNTNNGPVLSEFYQKVLDEFGAKKVDIVAHSMGANTPYITKN 120
DB 61 GWSRGKLYAVDFMDKGTGNTNNGPVLSEFYQKVLDEFGAKKVDIVAHSMGANTPYITKN 120
QY 121 LDGNGKIEENVYTLGAGNSTSKALPGTDPNOKILYISYSSADMIYNNYLSKIDGAKNA 180
DB 121 LDGNGKIEENVYTLGAGNSTSKALPGTDPNOKILYISYSSADMIYNNYLSKIDGAKNA 180
QY 181 QIHGVGHIGILMNSQVNSLIKEGLNGGQNTN 212
DB 181 QIHGVGHIGILMNSQVNSLIKEGLNGGQNTN 212
RESULT 3
AA083848
ID AA083848 standard; Protein: 212 AA.
AC AA083848;
XX
DT 08-MAY-2002 (first entry)
XX
DE Bacillus lipase polypeptide #8.
XX
KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
KW gastrointestinal.
XX
OS Bacillus badius.
XX
PN WO200206457-A2.
XX
PD 24-JAN-2002.
XX

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PF 13-JUL-2001; 2001WO-US22160.
XX
XX 13-JUL-2000; 2000US-217954P.
PR 21-JUN-2001; 2001US-300378P.
XX
XX (MAXY-) MAXYGEN INC.
PA
XX Giver LJ, Minshull J, Vogel K;
PI
XX WPI: 2002-171805/22.
DR N-PSDB; ARK33826.
XX
XX Nucleic acids encoding lipase enzymes which are useful as supplements
PT in animal feeds, as agents of flavour modification and for treating
PT Crohn's disease and coeliac disease -
XX
XX Claim 20; Page 139; 196pp; English.
XX
XX The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
CC polypeptides of the invention.
XX
XX Sequence 212 AA:
SQ
Query Match 97.7%; Score 1063; DB 23; Length 212;
Best Local Similarity 98.1%; Pred. No. 5.8e-101;
Matches 208; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKFVKRRRIALVTIILSVTSLFAMOPSAKAAEHNPVNVVHIGGASYNFAGIKSYLSQ 60
DB 1 MKFVKRRRIALVTIILSVTSLFAMOPSAKAAEHNPVNVVHIGGASYNFAGIKSYLSQ 60
QY 61 GMSRGLYAVDFWMDKTGTNYNNGPVLSPRVQVLDGTGAKKVDIYAHSMGANTPYITKN 120
DB 61 GMSRGLYAVDFWMDKTGTNYNNGPVLSPRVQVLDGTGAKKVDIYAHSMGANTPYITKN 120
QY 121 LDGKNKIEENVVTLGGANRSTSKALPGTDPNOKIILYTSYSSADMTVMYLSKLDGAKNA 180
DB 121 LDGKNKIEENVVTLGGANRSTSKALPGTDPNOKIILYTSYSSADMTVMYLSKLDGAKNA 180
QY 181 QIHGVGHIGLLMNSQVNSLIKEGLNGGQNTN 212
DB 181 QIHGVGHIGLLMNSQVNSLIKEGLNGGQNTN 212

RESULT 4
AAU83844
ID AAU83844 standard; Protein; 212 AA.
XX
XX AAU83844;
AC
XX 08-MAY-2002 (first entry)
DT
XX
XX Bacillus lipase polypeptide #4.
DE
XX
XX Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
KW gastrointestinal.
XX
XX Bacillus lentus.
OS

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XX
XX WO200206457-A2.
PN
XX
XX 24-JAN-2002.
PD
XX
XX 13-JUL-2001; 2001WO-US22160.
PF
XX
XX 13-JUL-2000; 2000US-217954P.
PR 21-JUN-2001; 2001US-300378P.
XX
XX (MAXY-) MAXYGEN INC.
PA
XX Giver LJ, Minshull J, Vogel K;
PI
XX WPI: 2002-171805/22.
DR N-PSDB; ARK33822.
XX
XX Nucleic acids encoding lipase enzymes which are useful as supplements
PT in animal feeds, as agents of flavour modification and for treating
PT Crohn's disease and coeliac disease -
XX
XX Claim 20; Page 138-139; 196pp; English.
XX
XX The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
CC polypeptides of the invention.
XX
XX Sequence 212 AA:
SQ
Query Match 97.5%; Score 1061; DB 23; Length 212;
Best Local Similarity 98.1%; Pred. No. 9.4e-101;
Matches 208; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKFVKRRRIALVTIILSVTSLFAMOPSAKAAEHNPVNVVHIGGASYNFAGIKSYLSQ 60
DB 1 MKFVKRRRIALVTIILSVTSLFAMOPSAKAAEHNPVNVVHIGGASYNFAGIKSYLSQ 60
QY 61 GMSRGLYAVDFWMDKTGTNYNNGPVLSPRVQVLDGTGAKKVDIYAHSMGANTPYITKN 120
DB 61 GMSRGLYAVDFWMDKTGTNYNNGPVLSPRVQVLDGTGAKKVDIYAHSMGANTPYITKN 120
QY 121 LDGKNKIEENVVTLGGANRSTSKALPGTDPNOKIILYTSYSSADMTVMYLSKLDGAKNA 180
DB 121 LDGKNKIEENVVTLGGANRSTSKALPGTDPNOKIILYTSYSSADMTVMYLSKLDGAKNA 180
QY 181 QIHGVGHIGLLMNSQVNSLIKEGLNGGQNTN 212
DB 181 QIHGVGHIGLLMNSQVNSLIKEGLNGGQNTN 212

RESULT 5
AAU83845
ID AAU83845 standard; Protein; 212 AA.
XX
XX AAU83845;
AC
XX 08-MAY-2002 (first entry)
DT
XX
XX Bacillus lipase polypeptide #5.
DE
XX
XX Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW

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KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; anti-inflammatory; respiratory;
KW gastrointestinal.
XX
OS Bacillus circulans.
XX
PN W0200206457-A2.
XX
PD 24-JAN-2002.
XX
PE 13-JUL-2001; 2001WO-US22160.
XX
PR 13-JUL-2000; 2000US-217954P.
XX
PR 21-JUN-2001; 2001US-300378P.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Glaver LJ, Minshull J, Vogel K;
XX
DR WPI; 2002-171805/22.
DR
DR N-PSDB; ABR33823.
XX
XX
PT Nucleic acids encoding lipase enzymes which are useful as supplements
PT in animal feeds, as agents of flavour modification and for treating
PT Crohn's disease and coeliac disease -
XX
PS Claim 20; Page 139; 196pp; English.
XX
XX The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AA083841-AA083897 represent Bacillus lipase
CC polypeptides of the invention.
XX
SQ Sequence 212 AA;
XX
Query Match 97.4%; Score 1060; DB 23; Length 212;
Best Local Similarity 97.6%; Pred. No. 1.2e-100;
Matches 207; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
XX
OY 1 MKFVKRRITIAVTLIVSVTSLEFAMOPSAKAAEHNPVVMVHGIGASYNFAGIKSYLVSO 60
DB 1 MKFVKRRITIAVTLIVSVTSLEFAMOPSAKAAEHNPVVMVHGIGASYNFAGIKSYLVSO 60
OY 61 GMSRGKLYAVDFMDKTGTNNYNGPVLSEFVOKVLDGTGAKKVDIVAHSMGANTPYIKN 120
DB 61 GMSRGKLYAVDFMDKTGTNNYNGPVLSEFVOKVLDGTGAKKVDIVAHSMGANTPYIKN 120
OY 121 LDGNGKLTENVVTLGGANSTTSKALPGTDPNOKILTYTSYSSADMTVWNTYLSKLDGAKNA 180
DB 121 LDGNGKLTENVVTLGGANSTTSKALPGTDPNOKILTYTSYSSADMTVWNTYLSKLDGAKNA 180
OY 181 QIHGVGHIGLIMNSOVNSLIKEGLNGGGLNTN 212
DB 181 QIHGVGHIGLIMNSOVNSLIKEGLNGGGLNTN 212

RESULT 6
AA083846
ID AA083846 standard; Protein: 212 AA.
XX
AC AA083846;
XX
DT 08-MAY-2002 (first entry)
XX

DE Bacillus lipase polypeptide #6.
XX
XX Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; anti-inflammatory; respiratory;
KW gastrointestinal.
XX
OS Bacillus azotoformans.
XX
PN W0200206457-A2.
XX
PD 24-JAN-2002.
XX
PE 13-JUL-2001; 2001WO-US22160.
XX
PR 13-JUL-2000; 2000US-217954P.
XX
PR 21-JUN-2001; 2001US-300378P.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Glaver LJ, Minshull J, Vogel K;
XX
DR WPI; 2002-171805/22.
DR
DR N-PSDB; ABR33824.
XX
XX
PT Nucleic acids encoding lipase enzymes which are useful as supplements
PT in animal feeds, as agents of flavour modification and for treating
PT Crohn's disease and coeliac disease -
XX
PS Claim 20; Page 139; 196pp; English.
XX
XX The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AA083841-AA083897 represent Bacillus lipase
CC polypeptides of the invention.
XX
SQ Sequence 212 AA;
XX
Query Match 96.2%; Score 1047; DB 23; Length 212;
Best Local Similarity 96.7%; Pred. No. 2.6e-99;
Matches 205; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
XX
OY 1 MKFVKRRITIAVTLIVSVTSLEFAMOPSAKAAEHNPVVMVHGIGASYNFAGIKSYLVSO 60
DB 1 MKFVKRRITIAVTLIVSVTSLEFAMOPSAKAAEHNPVVMVHGIGASYNFAGIKSYLVSO 60
OY 61 GMSRGKLYAVDFMDKTGTNNYNGPVLSEFVOKVLDGTGAKKVDIVAHSMGANTPYIKN 120
DB 61 GMSRGKLYAVDFMDKTGTNNYNGPVLSEFVOKVLDGTGAKKVDIVAHSMGANTPYIKN 120
OY 121 LDGNGKLTENVVTLGGANSTTSKALPGTDPNOKILTYTSYSSADMTVWNTYLSKLDGAKNA 180
DB 121 LDGNGKLTENVVTLGGANSTTSKALPGTDPNOKILTYTSYSSADMTVWNTYLSKLDGAKNA 180
OY 181 QIHGVGHIGLIMNSOVNSLIKEGLNGGGLNTN 212
DB 181 QIHGVGHIGLIMNSOVNSLIKEGLNGGGLNTN 212

RESULT 7
AA083849
ID AA083849 standard; Protein: 212 AA.

XX	AA083849;	
AC		
XX		
DT	08-MAY-2002 (first entry)	
XX		
DE	Bacillus lipase polypeptide #9.	
XX		
KW	lipase; Bacillus sp.	
KW	human foodstuff; cheese; food emulsifier; leather tanning; enzyme;	
KW	leather processing; cleaning agent; Crohn's disease; cystic fibrosis;	
KW	coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;	
KW	gastrointestinal lipid related condition; antiinflammatory; respiratory;	
KW	gastrointestinal.	
XX		
OS	Bacillus sp.	
XX		
PN	WO200206457-A2.	
XX		
PD	24-JAN-2002.	
XX		
PF	13-JUL-2001; 2001WO-US22160.	
XX		
PR	13-JUL-2000; 2000US-217954P.	
XX		
PR	21-JUN-2001; 2001US-300378P.	
XX		
PA	(MAXY-) MAXYGEN INC.	
XX		
PI	Gäiver LJ, Minshall J, Vogel K;	
XX		
DR	WPI: 2002-171805/22.	
XX		
DR	N-PSDB: ABR33827.	
XX		
PT	Nucleic acids encoding lipase enzymes which are useful as supplements	
XX	in animal feeds, as agents of flavour modification and for treating	
PT	Crohn's disease and coeliac disease -	
PS		
XX	Claim 32; Page 139; 196pp; English.	
XX		
CC	The invention relates to new Bacillus lipase enzymes and the nucleic	
CC	acids encoding them. The lipase polypeptides are useful as supplements	
CC	in animal feeds, as agents of flavour modification and fat modification in	
CC	human foodstuffs (e.g. cheese), as agents in the creation of food	
CC	emulsifiers, as agents for tanning/processing of leather and as cleaning	
CC	agents. They are also useful for treating Crohn's disease, cystic	
CC	fibrosis, coeliac disease, indigestion, obesity and other	
CC	gastrointestinal mal-absorption problems. Gastrointestinal lipid related	
CC	conditions can be therapeutically or prophylactically treated via a	
CC	method of hydrolysing a lipid comprising expressing in a target cell or	
CC	contacting a target cell with an effective amount of DNA or protein of	
CC	the invention. Sequences AA083841-AA083897 represent Bacillus lipase	
CC	polypeptides of the invention.	
XX		
XX		
SQ	Sequence 212 AA;	
	Query Match 92.6%; Score 1008; DB 23; Length 212;	
	Best Local Similarity 92.9%; Pred. No. 2.6e-95;	
	Matches 197; Conservative 7; Mismatches 8; Indels 0; Gaps 0;	
QY	1 MKFVKRIIALVTLLVLSVTSLEFAMQPSAKAEHNPVVMVHIGASVNFAGIKSYLSQ 60	
DB	1 MKFVKRIIALVTLLVLSVTSLEFALQPSAKAEHNPVVMVHIGASVNFAGIKSYLSQ 60	
QY	61 GMSRCKLAVDPFMDKTGNNYNNNGPVLRSFYQVLDDETGAKKVDIYAHSGGANTPIYYIN 120	
DB	61 GMSRCKLAVDPFMDKTGNNYNNNGPVLRSFYQVLDDETGAKKVDIYAHSGGANTPIYYIN 120	
QY	121 LDGNGKIEENVVTLTGANSSTSKALPGDPDNPCKILYTSIYSSADMIVMNYLSKLDGAKNA 180	
DB	121 LDGNGKIEENVVTLTGANSSTSKALPGDPDNPCKILYTSIYSSADMIVMNYLSKLDGAKNA 180	
QY	181 QIHGVGHIGLLMNSQVNSLKEGLNGGCGNTN 212	
DB	181 QIHGVGHIGLLYSSQVNSLKEGLNGGCGIANTN 212	

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RESULT 8
AAU83842
ID AAU83842 standard; Protein: 212 AA.
XX
XX AAU83842;
XX
XX 08-MAY-2002 (first entry)
XX
XX DE Bacillus lipase polypeptide #2.
XX
XX KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
XX KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
XX KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
XX KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
XX KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
XX KW gastrointestinal.
XX
XX OS Bacillus subtilis.
XX
XX PN WO200206457-A2.
XX
XX PD 24-JAN-2002.
XX
XX PF 13-JUL-2001; 2001WO-US22160.
XX
XX PR 13-JUL-2000; 2000US-217954P.
XX
XX PR 21-JUN-2001; 2001US-300378P.
XX
XX PA (MAXY-) MAXYGEN INC.
XX
XX PI Glaver LJ, Minshull J, Vogel K;
XX
XX DR WPI: 2002-171805/22.
XX
XX DR N-PSDB: ABRK33820.
XX
XX PT Nucleic acids encoding lipase enzymes which are useful as supplements
XX PT in animal feeds, as agents of flavour modification and for treating
XX PT Crohn's disease and coeliac disease -
XX
XX PS Claim 38; Page 138; 196pp; English.
XX
XX XX The invention relates to new Bacillus lipase enzymes and the nucleic
XX XX acids encoding them. The lipase polypeptides are useful as supplements
XX XX in animal feeds, as agents of flavour modification and fat modification in
XX XX human foodstuffs (e.g. cheese), as agents in the creation of food
XX XX emulsifiers, as agents for tanning/processing of leather and as cleaning
XX XX agents. They are also useful for treating Crohn's disease, cystic
XX XX fibrosis, coeliac disease, indigestion, obesity and other
XX XX gastrointestinal mal-absorption problems. Gastrointestinal lipid related
XX XX conditions can be therapeutically or prophylactically treated via a
XX XX method of hydrolysing a lipid comprising expressing in a target cell or
XX XX contacting a target cell with an effective amount of DNA or protein of
XX XX the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
XX XX polypeptides of the invention.
XX
XX SO Sequence 212 AA:
XX
XX
XX Query Match 92.6%; score 1007; DB 23; length 212;
XX Best Local Similarity 92.0%; Pred. No.3.3e-95;
XX Matches 195; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
XX
XX QY 1 MKFYARRIALVTILVLSVTSLEFAMQPSKAAEHNPVVMVHGIGASYNFAGIKSYLSQ 60
XX DB 1 MKFYARRIALVTILVLSVTSLEFALQPSKAAEHNPVVMVHGIGASYNFAGIKSYLSV 60
XX QY 61 GMSRRLKLAVDPMQDTGNNYNGPVLSPYQGVLDGTGAKKVDIAHSGANGFYYIKN 120
XX DB 61 GMSRRLKLAVDPMQDTGNNYNGPVLSPRYQGVLDGTGAKKVDIAHSGANGANTLYIKN 120
XX QY 121 LDGGKRIENVVTLGGANSTSTSKALPGTDPNOKILYTSIYSSADMIVMNYLSKLDGAKNA 180
XX DB 121 LDGGKRIENVVTLGGANSTSTSKALPGTDPNOKILYTSIYSSADMIVMNYLSKLDGAKNA 180

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Oy 1 MKFVKRRRIALVTLLVSVTSLEFAMOPSAKAAEHNPVWVHGIGASYNFAGIKSYLSQ 60
    |||
Db 1 MKFVKRRRIALVTLLVSVTSLEFALQPSAKAAEHNPVWVHGIGASYNFAGIKSYLSQ 60
Oy 61 GMSRCKLAVAVDWDKGTGTYNNNGPVLRSFYQVLDFTGAKKVDIYAHSGGANTPYIYN 120
    |||
Db 61 GMSRCKLAVAVDWDKGTGNNLNNGPVLRSFYKVLDETGAKKVDIYAHSGGANTLYIYN 120
Oy 121 LDGKNIENVVTLGGANRSTSKALPGTDPNOKIITVTSYSSADMTVMYLSKLDGAKNA 180
    |||
Db 121 LDGKNIENVVTLGGANRLVLTGKALPGTDPNOKIITVTSYSSADMTVMYLSKLDGAKNV 180
Oy 181 QIHGVGHIGLLMNSQVNSLIKEGLNGGONTN 212
    |||
Db 181 QIHGVGHIGLLYSQVNSLIKEGLNGGLNTN 212

RESULT 11
AU083856 standard; Protein; 212 AA.
AC AU083856;
XX
XX 08-MAY-2002 (first entry)
XX
XX Bacillus lipase polypeptide #16.
XX
XX Lipase; Bacillus; animal feed; flavour modification; fat modification;
XX human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
XX leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
XX coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
XX gastrointestinal lipid related condition; antiinflammatory; respiratory;
XX gastrointestinal.
XX
XX OS Bacillus sp.
XX
XX WO200206457-A2.
XX
XX 24-JAN-2002.
XX
XX 13-JUL-2001; 2001WO-US22160.
XX
XX 13-JUL-2000; 2000US-217954P.
XX
XX 21-JUN-2001; 2001US-300378P.
XX
XX (MAXY-) MAXYGEN INC.
XX
XX Giver LJ, Minshull J, Vogel K;
XX
XX WPI; 2002-171805/22.
XX
XX N-PSDB; ABR33834.
XX
XX Nucleic acids encoding lipase enzymes which are useful as supplements
XX in animal feeds, as agents of flavour modification and for treating
XX Crohn's disease and coeliac disease -
XX
XX Claim 32; Page 140; 196pp; English.
XX
XX The invention relates to new Bacillus lipase enzymes and the nucleic
XX acids encoding them. The lipase polypeptides are useful as supplements in
XX animal feeds, as agents of flavour modification and fat modification in
XX human foodstuffs (e.g. cheese), as agents in the creation of food
XX emulsifiers, as agents for tanning/processing of leather and as cleaning
XX agents. They are also useful for treating Crohn's disease, cystic
XX fibrosis, coeliac disease, indigestion, obesity and other
XX gastrointestinal mal-absorption problems. Gastrointestinal lipid related
XX conditions can be therapeutically or prophylactically treated via a
XX method of hydrolysing a lipid comprising expressing in a target cell or
XX contacting a target cell with an effective amount of DNA or protein of
XX the invention. Sequences AU083841-AU083897 represent Bacillus lipase
XX polypeptides of the invention.
XX
XX Sequence 212 AA:

```

```

Query Match          91.2%; Score 992; DB 23; Length 212;
Best Local Similarity 92.0%; Pred No. 1.2e-93;
Matches 195; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Oy 1 MKFVKRRRIALVTLLVSVTSLEFAMOPSAKAAEHNPVWVHGIGASYNFAGIKSYLSQ 60
    |||
Db 1 MKFVKRRRIALVTLLVSVTSLEFALQPSAKAAEHNPVWVHGIGASYNFAGIKSYLSQ 60
Oy 61 GMSRCKLAVAVDWDKGTGTYNNNGPVLRSFYQVLDFTGAKKVDIYAHSGGANTPYIYN 120
    |||
Db 61 GMSRCKLAVAVDWDKGTGNNLNNGPVLRSFYKVLDETGAKKVDIYAHSGGANTLYIYN 120
Oy 121 LDGKNIENVVTLGGANRSTSKALPGTDPNOKIITVTSYSSADMTVMYLSKLDGAKNA 180
    |||
Db 121 LDGKNIENVVTLGGANRLVLTGKALPGTDPNOKIITVTSYSSADMTVMYLSKLDGAKNV 180
Oy 181 QIHGVGHIGLLMNSQVNSLIKEGLNGGONTN 212
    |||
Db 181 QIHGVGHIGLLYSQVNSLIKEGLNGGLNTN 212

RESULT 12
AU083854 standard; Protein; 212 AA.
AC AU083854;
XX
XX 08-MAY-2002 (first entry)
XX
XX Bacillus lipase polypeptide #14.
XX
XX Lipase; Bacillus; animal feed; flavour modification; fat modification;
XX human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
XX leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
XX coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
XX gastrointestinal lipid related condition; antiinflammatory; respiratory;
XX gastrointestinal.
XX
XX OS Bacillus sp.
XX
XX WO200206457-A2.
XX
XX 24-JAN-2002.
XX
XX 13-JUL-2001; 2001WO-US22160.
XX
XX 13-JUL-2000; 2000US-217954P.
XX
XX 21-JUN-2001; 2001US-300378P.
XX
XX (MAXY-) MAXYGEN INC.
XX
XX Giver LJ, Minshull J, Vogel K;
XX
XX WPI; 2002-171805/22.
XX
XX N-PSDB; ABR33832.
XX
XX Nucleic acids encoding lipase enzymes which are useful as supplements
XX in animal feeds, as agents of flavour modification and for treating
XX Crohn's disease and coeliac disease -
XX
XX Claim 30; Page 140; 196pp; English.
XX
XX The invention relates to new Bacillus lipase enzymes and the nucleic
XX acids encoding them. The lipase polypeptides are useful as supplements in
XX animal feeds, as agents of flavour modification and fat modification in
XX human foodstuffs (e.g. cheese), as agents in the creation of food
XX emulsifiers, as agents for tanning/processing of leather and as cleaning
XX agents. They are also useful for treating Crohn's disease, cystic
XX fibrosis, coeliac disease, indigestion, obesity and other
XX gastrointestinal mal-absorption problems. Gastrointestinal lipid related
XX conditions can be therapeutically or prophylactically treated via a
XX method of hydrolysing a lipid comprising expressing in a target cell or

```

CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AA083841-AA083897 represent Bacillus lipase
CC polypeptides of the invention.

SO Sequence 212 AA;

Query Match 90.9%; Score 989; DB 23; Length 212;
Best Local Similarity 91.5%; Pred. No. 2,4e-93;
Matches 194; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 MKFVRRRIIAVTLVLTSLFAMQPSAKAEHNPVWVHVGIGASYNFAGIKSYLSQ 60
DB 1 MKFVRRRIIAVTLVLTSLFAMQPSAKAEHNPVWVHVGIGASYNFAGIKSYLSQ 60
QY 61 GMSRCKLYAVDFWMDKTGTYNNGPVLRSFVQVLDGTGAKKVDIVAHSMGANTPYITKN 120
DB 61 GMSRCKLYAVDFWMDKTGTYNNGPVLRSFVQVLDGTGAKKVDIVAHSMGANTPYITKN 120
QY 121 LDGKKIENVVTLGGANRLVTKALPGTDPNOKILYTSVSSADMI VMNYLTAKLDGAKNV 180
DB 121 LDGKKIENVVTLGGANRLVTKALPGTDPNOKILYTSVSSADMI VMNYLTAKLDGAKNV 180
QY 181 QIHGVGHIGLMSQVNSLIKEGLNGGQNTN 212
DB 181 QIHGVGHIGLMSQVNSLIKEGLNGGQNTN 212

RESULT 13

AA083894
ID AA083894 standard; Protein; 180 AA.

AC AA083894;

DT 08-MAY-2002 (first entry)

DE Bacillus lipase polypeptide #54.

XX Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
KW gastrointestinal.

OS Synthetic.

PN WO200206457-A2.

PD 24-JAN-2002.

PE 13-JUL-2001; 2001WO-US22160.

PF 13-JUL-2000; 2000US-217954P.

PR 21-JUN-2001; 2001US-300378P.

PS (MAXY-) MAXYGEN INC.

PI Giver LJ, Minshull J, Vogel K;

PT WPI; 2002-171805/22.

DR N-PSDB; ABK33872.

XX Nucleic acids encoding lipase enzymes which are useful as supplements

PT in animal feeds, as agents of flavour modification and for treating

PT Crohn's disease and coeliac disease -

PS Claim 5; Page 145-146; 196pp; English.

XX The invention relates to new Bacillus lipase enzymes and the nucleic

CC acids encoding them. The lipase polypeptides are useful as supplements

CC in animal feeds, as agents of flavour modification and fat modification in

CC human foodstuffs (e.g. cheese), as agents in the creation of food

CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AA083841-AA083897 represent Bacillus lipase
CC polypeptides of the invention.

SO Sequence 180 AA;

Query Match 85.0%; Score 925; DB 23; Length 180;
Best Local Similarity 90.3%; Pred. No. 7e-87;
Matches 177; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 33 EHNPPVWVHVGIGASYNFAGIKSYLSVSGMSRGLYAVDFWMDKTGTYNNGPVLRSFVQ 92
DB 1 EHNPPVWVHVGIGASYNFAGIKSYLSVSGMSRGLYAVDFWMDKTGTYNNGPVLRSFVQ 92
QY 93 VLDETGAARKVDIVAHSMGANTPYITKNLDGKKNKENNVTLGGANRSTSKALPGTDPNQ 152
DB 93 VLDETGAARKVDIVAHSMGANTPYITKNLDGKKNKENNVTLGGANRSTSKALPGTDPNQ 152
QY 153 KILYTSVSSADMTVMNYLSKLDGAKKNOIHGVGHIGLMSQVNSLIKEGLNGGQNTN 212
DB 121 KILYTSVSSADMTVMNYLSKLDGAKKNOIHGVGHIGLMSQVNSLIKEGLNGGQNTN 212

RESULT 14

AA083890
ID AA083890 standard; Protein; 180 AA.

AC AA083890;

DT 08-MAY-2002 (first entry)

DE Bacillus lipase polypeptide #50.

XX Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
KW gastrointestinal.

OS Synthetic.

PN WO200206457-A2.

PD 24-JAN-2002.

PE 13-JUL-2001; 2001WO-US22160.

PF 13-JUL-2000; 2000US-217954P.

PR 21-JUN-2001; 2001US-300378P.

PS (MAXY-) MAXYGEN INC.

PI Giver LJ, Minshull J, Vogel K;

PT WPI; 2002-171805/22.

DR N-PSDB; ABK33868.

XX Nucleic acids encoding lipase enzymes which are useful as supplements

PT in animal feeds, as agents of flavour modification and for treating

PT Crohn's disease and coeliac disease -

PS Claim 5; Page 145; 196pp; English.

XX The invention relates to new Bacillus lipase enzymes and the nucleic

CC acids encoding them. The lipase polypeptides are useful as supplements

CC in animal feeds, as agents of flavour modification and fat modification in

CC human foodstuffs (e.g. cheese), as agents in the creation of food

CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
CC polypeptides of the invention.

SQ Sequence 180 AA:

Query Match

Best Local Similarity 97.8%; Score 921; DB 23; Length 180;

Matches 176; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 33 EHNPPVVMHIGIGASYNFAGIKSYLVSGWSRGLYAVDFWDXGTGNNNGPVLSPRVOK 92
DB 1 EHNPPVVMHIGIGASYNFAGIKSYLVSGWSRGLYAVDFWDXGTGNNNGPVLSPRVOK 60

QY 93 VLDGTGAKKVDIYAHSMGANTPYITKNDGKKIENVVTLGGANSTTSKALPGTDPNQ 152
DB 61 VLDGTGAKKVDIYAHSMGANTLYITKNDGKKIENVVTLGGANSTTSKALPGTDPNQ 120

QY 153 KILYTSYSSADMIVMNYLSKLDGAKNAOIHGVBHIGLLMNSOVNSLIKEGLNGGGONTN 212
DB 121 KILYTSYSSADMIVMNYLSKLDGAKNAOIHGVBHIGLLMNSOVNSLIKEGLNGGGONTN 180

RESULT 15

AAU83884
ID AAU83884 standard; Protein; 180 AA.

AC AAU83884;

DT 08-MAY-2002 (first entry)

DE Bacillus lipase polypeptide #44.

XX Lipase; Bacillus; animal feed; flavour modification; fat modification;
XX human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
XX leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
XX coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
XX gastrointestinal lipid related condition; anti-inflammatory; respiratory;
XX gastrointestinal.

OS Synthetic.

PN WO200206457-A2.

PD 24-JAN-2002.

PF 13-JUL-2001; 2001WO-US22160.

PR 13-JUL-2000; 2000US-217954P.

PR 21-JUN-2001; 2001US-300378P.

PA (MAXY-) MAXYGEN INC.

PI Giver LJ, Minshall J, Vogel K;

DR WPI; 2002-171805/22.

DR N-PSDB; ABR33862.

PT Nucleic acids encoding lipase enzymes which are useful as supplements
PT in animal feeds, as agents of flavour modification and for treating
PT Crohn's disease and coeliac disease -

PS Claim 5; Page 144; 196pp; English.

XX The invention relates to new Bacillus lipase enzymes and the nucleic
XX acids encoding them. The lipase polypeptides are useful as supplements in
XX animal feeds, as agents of flavour modification and fat modification in

CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
CC polypeptides of the invention.

SQ Sequence 180 AA:

Query Match

Best Local Similarity 97.2%; Score 918; DB 23; Length 180;

Matches 175; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 33 EHNPPVVMHIGIGASYNFAGIKSYLVSGWSRGLYAVDFWDXGTGNNNGPVLSPRVOK 92
DB 1 EHNPPVVMHIGIGASYNFAGIKSYLVSGWSRGLYAVDFWDXGTGNNNGPVLSPRVOK 60

QY 93 VLDGTGAKKVDIYAHSMGANTPYITKNDGKKIENVVTLGGANSTTSKALPGTDPNQ 152
DB 61 VLDGTGAKKVDIYAHSMGANTLYITKNDGKKIENVVTLGGANSTTSKALPGTDPNQ 120

QY 153 KILYTSYSSADMIVMNYLSKLDGAKNAOIHGVBHIGLLMNSOVNSLIKEGLNGGGONTN 212
DB 121 KILYTSYSSADMIVMNYLSKLDGAKNAOIHGVBHIGLLMNSOVNSLIKEGLNGGGONTN 180

Search completed: May 9, 2003, 16:20:58

Job time : 36 secs

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GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2003, 16:20:26 ; Search time 14 Seconds
(without alignments)
445.547 Million cell updates/sec

Title: US-09-905-666A-55
Perfect score: 1088
Sequence: 1 MKFVKRRRIALVTILVLSVT.....NSQVNSLIKEGLNGCGQNTN 212

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	798.5	73.4	213	1 US-07-930-678-2	Sequence 2, Appli
2	139.5	12.8	358	1 US-08-034-650-10	Sequence 10, Appli
3	139.5	12.8	358	1 US-08-449-015-10	Sequence 10, Appli
4	123	11.3	363	3 US-08-978-589A-2	Sequence 2, Appli
5	122	11.2	363	4 US-09-336-601-1	Sequence 1, Appli
6	114	10.5	364	1 US-08-400-422-3	Sequence 3, Appli
7	97.5	9.0	292	4 US-09-134-001C-3301	Sequence 3301, Ap
8	92	8.5	699	4 US-09-134-001C-4054	Sequence 4054, Ap
9	91.3	8.4	690	4 US-09-134-001C-4568	Sequence 4568, Ap
10	88	8.1	213	1 US-08-104-445-3	Sequence 3, Appli
11	87.5	8.0	313	3 US-08-732-412-2	Sequence 2, Appli
12	87.5	8.0	388	1 US-08-232-519-2	Sequence 2, Appli
13	87.5	8.0	388	1 US-08-456-956-2	Sequence 2, Appli
14	87	8.0	652	4 US-09-134-001C-3517	Sequence 3517, Ap
15	86.5	8.0	277	3 US-09-111-556A-3	Sequence 3, Appli
16	86.5	8.0	277	3 US-08-360-758-3	Sequence 3, Appli
17	86	7.9	535	3 US-08-286-870A-6	Sequence 6, Appli
18	86	7.9	648	3 US-08-286-870A-4	Sequence 4, Appli
19	86	7.9	719	3 US-08-286-870A-8	Sequence 8, Appli
20	85	7.8	262	2 US-08-602-359A-35	Sequence 35, Appli
21	85	7.8	3729	2 US-08-804-227C-4	Sequence 4, Appli
22	83.5	7.7	264	4 US-09-134-001C-5592	Sequence 5592, Ap
23	82.5	7.6	640	4 US-09-509-814A-6	Sequence 8, Appli
24	82.5	7.6	640	4 US-09-509-814A-8	Sequence 8, Appli
25	82	7.5	178	1 US-08-044-621D-32	Sequence 32, Appli
26	82	7.5	178	1 US-08-709-912-15	Sequence 15, Appli
27	82	7.5	178	2 US-09-047-370-15	Sequence 15, Appli

28	82	7.5	671	2 US-08-737-716-13	Sequence 13, Appli
29	81.5	7.5	275	6 5472855-5	Patent No. 5472855
30	81.5	7.5	551	4 US-09-615-192A-348	Sequence 348, App
31	81	7.4	312	4 US-09-134-001C-3465	Sequence 3465, Ap
32	81	7.4	1073	4 US-09-206-942-49	Sequence 49, Appli
33	81	7.4	1073	4 US-09-206-942-47	Sequence 47, Appli
34	80.5	7.4	284	4 US-09-134-001C-2927	Sequence 2927, Ap
35	80	7.4	316	1 US-07-828-980A-2	Sequence 2, Appli
36	80	7.4	539	4 US-09-036-987A-11	Sequence 11, Appli
37	80	7.4	539	4 US-09-370-700-11	Sequence 11, Appli
38	78.5	7.2	1426	4 US-09-136-574A-43	Sequence 43, Appli
39	78	7.2	340	4 US-09-134-001C-4056	Sequence 4056, Ap
40	78	7.2	366	4 US-09-134-001C-4412	Sequence 4412, Ap
41	78	7.2	371	3 US-08/622	INFORMATION FOR
42	78	7.2	371	4 US-09-165-922A-10	Sequence 10, Appli
43	78	7.2	503	4 US-09-562-737-64	Sequence 64, Appli
44	78	7.2	1104	4 US-09-268-347-28	Sequence 28, Appli
45	78	7.2	1104	4 US-09-268-347-34	Sequence 34, Appli

ALIGNMENTS

RESULT 1
US-07-930-678-2
Sequence 2, Application US/07930678
Patent No. 5427936
GENERAL INFORMATION:
APPLICANT: MOELLER, Bernhard
APPLICANT: VETTER, Roman
APPLICANT: WILKE, Detlef
APPLICANT: FOULLOIS, Birgit
TITLE OF INVENTION: Alkaline Bacillus Lipases, Coding DNA
TITLE OF INVENTION: Sequences thereof and Bacilli, Whichch Produce These
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/930,678
FILING DATE: 19921013
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP91/00664
FILING DATE: 08-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 40 12 070.8
FILING DATE: 14-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, J.D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 16877/318/KACH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-930-678-2

Db 61 KEANVVDIWKIGQSDLOSHG---AKYVYANLSGFQSDGPN-GRGEQLLAYVKQVLAATG 116

QY 99 AKKVDIVAHSMGGANTPYIKNLDGKGNKIENVYTLGGANST 140

Db 117 ATKVNLIGHSGGLTSRYVA--AVAPOLVASVTITGTPHRGS 156

RESULT 4

US-08-978-589A-2

Sequence 2, Application US/08978589A

Patent No. 6087145

GENERAL INFORMATION:

APPLICANT: ISHII, Takeshi

APPLICANT: MITSUDA, Satoshi

TITLE OF INVENTION: ESTERASE GENE AND ITS USE

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP

STREET: P.O. BOX 747

CITY: FALLS CHURCH

STATE: VIRGINIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 22040

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/978,589A

FILING DATE: 26-NOV-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murphy Jr., Gerald M.

REGISTRATION NUMBER: 28,977

REFERENCE/DOCKET NUMBER: 20-4336P

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 363 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-978-589A-2

Query Match 11.3%; Score 123; DB 3; Length 363;
Best Local Similarity 27.0%; Pred. No. 3.6e-05;
Matches 43; Conservative 27; Mismatches 59; Indels 30; Gaps 9;

QY 13 TILVLSVTSLEFAMQPSAK-----AAEHNPVYVNHGIGASYNFAGIKSYLSQGSRR--- 64

Db 26 TVLWMSLAGAQAASATAVDDYATRYPIILVHGLTGTD-KYGGVVEY-----WYRIPE 79

QY 65 -----GKLYAVD---FMDKTGTNNNGPVLRSFQKVLDETGAKKVDVAHSGKANTP 115

Db 80 DIRAHGAAYVYANLSGFOSDDGPN-GRGEQLLAFVKQYLAATGAQKVNLIHSGGL-TS 137

QY 116 YIKNLDCGNKIENVYTLG-----GANRSTTSKALPGTDP 150

Db 138 RYVASV-APELVASVTITSTPHWGSQFADFVQQLLOTDP 175

RESULT 5

US-09-336-601-1

Sequence 1, Application US/09336601

Patent No. 6184008

GENERAL INFORMATION:

APPLICANT: OHTA, Hiromichi

APPLICANT: SUGAI, Takeshi

APPLICANT: ISHII, Takeshi

APPLICANT: MITSUDA, Satoshi

TITLE OF INVENTION: PRODUCTION OF OPTICALLY ACTIVE SPHINGOID COMPOUND

FILE REFERENCE: 2185-349P

CURRENT APPLICATION NUMBER: US/09/336,601

CURRENT FILING DATE: 1999-06-21
EARLIER APPLICATION NUMBER: 09/034,007
EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 363

TYPE: PRT

ORGANISM: E. coli JM 109/pAL 612 strain

US-09-336-601-1

Query Match

Best Local Similarity 11.2%; Score 122; DB 4; Length 363;
Best Local Similarity 25.0%; Pred. No. 4.6e-05;

Matches 45; Conservative 32; Mismatches 61; Indels 42; Gaps 10;

QY 4 VKRRIALVTILVL-----SVTSLEFAMQPSAK-----AAEHNPVYVNHGIGCA 46

Db 5 IRKAVATVVAITAMNAPASVGTLSLAGAQAASATAVDDYATRYPIILVHGLTGT 64

QY 47 SYNFAKISYLSQGSRR-----GKLYAVD---FMDKTGTNNNGPVLRSFQKVL 94

Db 65 D-KYGGVVEY-----WYRIPELRAHGAAYVYANLSGFOSDDGPN-GRGEQLLAFVKQYL 117

QY 95 DETGAKKVDVAHSGKANTPYIKNLDCGNKIENVYTLG-----GANRSTTSKALPGTDP 150

Db 118 AATGAQKVNLIHSGGL-TSRYVASV-APELVASVTITSTPHWGSQFADFVQQLLOTDP 175

RESULT 6

US-08-400-422-3

Sequence 3, Application US/08400422

Patent No. 5681715

GENERAL INFORMATION:

APPLICANT: Jorgensen, Steen Troels

APPLICANT: Diderichsen, Boerge Krag

APPLICANT: Buckley, Catherine M.

APPLICANT: Hobson, Audrey

APPLICANT: McConnell, David J.

TITLE OF INVENTION: A process for the preparation of an active

TITLE OF INVENTION: Lipase

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 56817150 No. 5681715disk of No. 5681715th America, Inc.

STREET: 405 Lexington Avenue, 62nd floor

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10174-6201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/400,422

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/038,763

FILING DATE: 25-MAR-1993

APPLICATION NUMBER: PCT/DK91/00402

FILING DATE: 20-DEC-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/DK92/00391

FILING DATE: 18-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J.

REGISTRATION NUMBER: 33,728

REFERENCE/DOCKET NUMBER: 3663.200-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 867 0123

TELEFAX: 212 867 0298

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Pseudomonas cepacia
STRAIN: DSM 3401
US-08-400-422-3

Query Match 10.5%; Score 114; DB 1; Length 364;
Best Local Similarity 25.9%; Pred. No. 0.00035;
Matches 42; Conservative 27; Mismatches 59; Indels 34; Gaps 8;

QY 4 VKRILALVTLVLSV-----TSLFAMQPSAKAEH---NPVYVHGIGCA 46
DB 5 MRSYVAGAAVACAMVAPFAGATAVMTLATTHAAMATAPDDYATRRYPIILVHGLGT 64
QY 47 SYNFAKISKY-----LVSGMSRGKLYAVD---FMDKTGTYNNNGPVLSPFYOKVLDE 96
DB 65 D-KYAGVLEHYGYIOEDLQOHG---ATVYVANLSGFQSDGPN-GRGEQLATVYKTVLAA 119
QY 97 TGAKKVDIVAHSMGANTPYIKNLGDKNKIENVYTLGKANR 138
DB 120 TGATKVNILVGHXGGLTSRYVA--AVAADLIVASVTITGTPHR 159

RESULT 7
US-09-134-001C-3301
Sequence 3301, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3301
LENGTH: 292
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3301

Query Match 9.0%; Score 97.5; DB 4; Length 292;
Best Local Similarity 19.9%; Pred. No. 0.016;
Matches 48; Conservative 38; Mismatches 90; Indels 65; Gaps 9;

QY 13 TILVLSV-----TSLFAMQPSAKAEHNPVYVHGIGASYNFAGIKSYLVSGW--- 62
DB 20 TVLVLIIVNKTOSQSYISTHYSNNKIKTTATLFLHGYGGSERS---ETPMQALNKN 75
QY 63 -----SRGKLY-----AVDFMD-KITNTNNNGPVLSPFYOKVLDE 96
DB 76 VTNEVITARVSSSEKVFYFDRKLSDDAANPIYKVEFKDKTKFNEMVWIKEVLSQLKSQ 135
QY 97 TGAKKVDIVAHSMGANTPYIKNLGDKN---KIENVYTLGK-----ANRSTTS 142
DB 136 FGIOGFNFVGHSMGNISFAFMKMYGDDRHLPOLAKKEVNIAGVYNGILNMENVEIIVD 195
QY 143 KALPGTDPN---OKILYTSIYSSADMIVMNYLSKLDGAKNAQIHGVGHIGLILNNSOVNS 198
DB 196 KQGPFRHMNAAYRQLLSLYKIKYCGKEIFVLNIYGDLEDGSHSD-----GRVSNSSSQS 248

QY 199 L 199
DB 249 L 249

RESULT 8
US-09-134-001C-4054
Sequence 4054, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4054
LENGTH: 699
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4054

Query Match 8.5%; Score 92; DB 4; Length 699;
Best Local Similarity 19.7%; Pred. No. 0.23;
Matches 46; Conservative 37; Mismatches 60; Indels 90; Gaps 11;

QY 28 SAKAEH---NPVYVHGIGASYNFAGIKSYLVSGWSRKL-----YAVD 71
DB 312 SAKQKYNNDPIILVHGFNGETDD---INPSVLTHWGGDKMIRKODLENGYEAVEAS 368
QY 72 FMDKTGTYNNNGPVLSPFYOKVLDEGTA-----KKVDIVA 106
DB 369 I-SAFGSIYDAVLELYIYIKGRVDYGAHAHAKYGERYKTYGGYKKMKPGKIHILG 427
QY 107 HSMGANTPYIKNL-----GG--NKIENVYTLGKANR 138
DB 428 HSMGQGT---IROLEELRHGNEPEVEYQKOHGEISPLFGGHDNMVSSITTLGTPHN 483
QY 139 STSKALPGTDPNOKILYTSIYSSADMIVMNYLSKLDGAKNAQI-HGVGHIGL 190
DB 484 GTHASDLG---NEAIVROLAYD-----VGMKGNKDSRVDFGLEHWGL 524

RESULT 9
US-09-134-001C-4568
Sequence 4568, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4568
LENGTH: 690
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4568

Query Match 8.4%; Score 91.5; DB 4; Length 690;
Best Local Similarity 20.4%; Pred. No. 0.26;
Matches 54; Conservative 32; Mismatches 72; Indels 107; Gaps 12;

Db 121 AAVRP--DLVAVSYVSGAPHK-----GSPDTADFIQIPPGSGAGEAIVAGI----- 163

QY 178 KNAQIHGVGHI-----GLMNSQVNSL-IRKGLNGCG 208

Db 164 ----VNGIGALINFLSGSSSTSPONALCALSLNSEG 196

RESULT 12

US-08-232-519-2

; Sequence 2, Application US/08232519

; Patent No. 5484725

; GENERAL INFORMATION:

; APPLICANT: Kageyama, Bunji

; APPLICANT: Nakae, Masanori

; APPLICANT: Yaqui, Shigeo

; TITLE OF INVENTION: NORBORANE TYPE ESTER HYDROLASE

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10020

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/232,519

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 5-96286

; FILING DATE: 22-APR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Haley Jr, James F

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: SHGN-4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 596-9000

; TELEFAX: (212) 596-9090

; TELEX: 14-8367

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 388 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-232-519-2

Query Match 8.0%; Score 87.5; DB 1; Length 388;

Best Local Similarity 23.1%; Pred. No. 0.3;

Matches 40; Conservative 34; Mismatches 60; Indels 39; Gaps 8;

QY 33 EHNPNVAVHVGIGASYNAGIKSYVSG--WSRGLYAVDFMDKGTNNYNG---PVL 86

Db 134 EGTPIVLVHGFSG-----DISNMWLTODALAERRVIAFDLPCHGASSKNVGTGTLAFL 187

QY 87 SRFVQKVLDETGAKKVDIVAHSMGA-----NTPYIRKND-----GKNKIENVVTLG 134

Db 188 AGVYSELLQTIKIEKAHVHSGGIALTLRLRHPDQVASINLAPGLGKDVADPIS 247

QY 135 GANSTSTKALPGDTPNCKILYTSYSSA-----DMIVMNYLSKLDGAKNA 180

Db 248 AFVSESSSRDM-----KAVLQMLVYNKALVGRKKVDAVLR--ARRLDGARDA 292

RESULT 13

US-08-456-956-2

; Sequence 2, Application US/08456956

; Patent No. 5686285

; GENERAL INFORMATION:

; APPLICANT: Kageyama, Bunji

; APPLICANT: Nakae, Masanori

; APPLICANT: Yaqui, Shigeo

; TITLE OF INVENTION: No. 5686285borane Type Ester Hydrolase

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10020

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/456,956

; FILING DATE: 01-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 5-96286

; FILING DATE: 22-APR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/232,519

; FILING DATE: 22-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Haley Jr, James F

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: SHGN-4 DIV 1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)596-9000

; TELEFAX: (212)596-9090

; TELEX: 14-8367

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 388 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-456-956-2

Query Match 8.0%; Score 87.5; DB 1; Length 388;

Best Local Similarity 23.1%; Pred. No. 0.3;

Matches 40; Conservative 34; Mismatches 60; Indels 39; Gaps 8;

QY 33 EHNPNVAVHVGIGASYNAGIKSYVSG--WSRGLYAVDFMDKGTNNYNG---PVL 86

Db 134 EGTPIVLVHGFSG-----DISNMWLTODALAERRVIAFDLPCHGASSKNVGTGTLAFL 187

QY 87 SRFVQKVLDETGAKKVDIVAHSMGA-----NTPYIRKND-----GKNKIENVVTLG 134

Db 188 AGVYSELLQTIKIEKAHVHSGGIALTLRLRHPDQVASINLAPGLGKDVADPIS 247

QY 135 GANSTSTKALPGDTPNCKILYTSYSSA-----DMIVMNYLSKLDGAKNA 180

Db 248 AFVSESSSRDM-----KAVLQMLVYNKALVGRKKVDAVLR--ARRLDGARDA 292

RESULT 14

US-09-134-001C-3517

; Sequence 3517, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucelle-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US-60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3517
LENGTH: 652
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3517

Query Match

8.0%; Score 87; DB 4; Length 652;

Best Local Similarity 21.4%; Pred. No. 0.74;
Matches 47; Conservative 24; Mismatches 63; Indels 86; Gaps 11;

QY 26 OPSAKAEHN--PYVMVGI-----GASVNFAGIKSYLVSGWSRGKL 67
DB 260 QLTNAQYKKNQPVYFVHGFVGLVEDAFSMYPNMGKRYN---VKQELTLGTRVHA 316
QY 68 YAVDFMDTGTNYNNGPVLSRFVQKVLDETA-----KRV 102
DB 317 NVGAF-----SSNYDRAVELYXIKGRVDYGAHAHAKYGHKRYGTYEGIMPDWEGKKI 372
QY 103 DIVASHMGGAN--TPYIKN-----LDG--NKIENVVTIGANR 138
DB 373 HLVGSHMGGQTRLMHEHLRNGNDEIDYQRYGTVSDLFKGGODNMVSTTLTLPN 432
QY 139 STSKALPGTDPNOKILYTSYSSADMIWNYLSKLDGAK 178
DB 433 GT-----PAAD---KLGTSTFKID---TINRIGIKGTRK 460

RESULT 15

US-09-111-556A-3

Sequence 3, Application US/09111556A

Patent No. 6020180

GENERAL INFORMATION:

APPLICANT: Svendsen, Allan

APPLICANT: Patnar, Shamkant A

APPLICANT: Egel-Mitani, Michi

APPLICANT: Borch, Kim

APPLICANT: Clausen, Ib G

APPLICANT: Hansen, Mogens T

TITLE OF INVENTION: C. ANTARCTICA LIPASE AND LIPASE VARIANTS

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6020180c No. 6020180disk of No. 6020180ch America, Inc.

STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Tape

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/111,556A

FILING DATE: 22-DEC-1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DK PCT/DK93/00225

FILING DATE: 03-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J.

REGISTRATION NUMBER: 33,728

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 277 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-111-556A-3

Query Match

8.0%; Score 86.5; DB 3; Length 277;

Best Local Similarity 26.4%; Pred. No. 0.23;
Matches 29; Conservative 21; Mismatches 49; Indels 11; Gaps 4;

QY 36 PYVMVHIGI-----GASVNFAGIKSYLVSGWSRGKLAVDFMDTGTNYNNGPVLSRFV 90
DB 10 PILLVHGLFGFDRIGSHHYFHGKIQALNECGAS---VFVPIISAANDEARGDILKQI 65
QY 91 QKVLDETGAKKYDIVAHSWGANFTPYIKNLDGKNKIEENVTLGGANRST 140
DB 66 HMLRQVGAQRVNLIGHSO-GALTRARYAAT-APELIASVTSVSGPNHGS 113

Search completed: May 9, 2003, 16:22:45

Job time : 16 secs

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GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2003, 16:22:01 ; Search time 20 Seconds
(without alignments)
975.473 Million cell updates/sec

Title: US-09-905-666a-55

Perfect score: 1088

Sequence: 1 MKFVKRRRIALVTILVSVT.....NSQVNSLIKEGLNGGONTN 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 349150 seqs, 92025710 residues

Total number of hits satisfying chosen parameters: 349150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/2/pubpaa/PTCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1060	97.4	212	US-10-028-247-4	Sequence 4, Appl1
2	136	14.3	324	US-09-738-626-3593	Sequence 3593, Ap
3	130	11.9	300	US-09-738-626-3594	Sequence 3594, Ap
4	123	11.3	363	US-10-147-467-2	Sequence 2, Appl1
5	101.5	9.3	299	US-10-080-644-6	Sequence 6, Appl1
6	92.5	8.5	1062	US-09-815-242-5111	Sequence 5111, Ap
7	89.5	8.2	308	US-10-080-644-8	Sequence 8, Appl1
8	88	8.1	311	US-09-815-242-11886	Sequence 11886, A
9	87.5	8.0	464	US-09-912-020-281	Sequence 281, App
10	87	8.0	315	US-10-098-174-1	Sequence 1, Appl1
11	86.5	8.0	518	US-10-080-644-2	Sequence 2, Appl1
12	86.5	8.0	690	US-09-815-242-5841	Sequence 5841, Ap
13	85	7.8	262	US-10-027-805-35	Sequence 35, Appl1
14	85	7.8	262	US-10-027-804-35	Sequence 35, Appl1
15	85	7.8	262	US-09-903-410-35	Sequence 35, Appl1
16	85	7.8	1023	US-09-884-696-5	Sequence 5, Appl1
17	82.5	7.6	259	US-09-738-626-3604	Sequence 3604, Ap
18	80.5	7.4	379	US-09-813-408-12	Sequence 12, Appl1
19	80	7.4	350	US-10-108-605-65	Sequence 65, Appl1

20	79	7.3	235	US-09-533-029-74	Sequence 74, Appl1
21	79	7.3	836	US-09-858-525A-10	Sequence 10, Appl1
22	79	7.3	871	US-09-858-525A-2	Sequence 2, Appl1
23	79	7.3	1463	US-09-971-536-69	Sequence 69, Appl1
24	78	7.2	503	US-10-211-962-64	Sequence 64, Appl1
25	77.5	7.1	495	US-10-213-990-42	Sequence 42, Appl1
26	77.5	7.1	1093	US-09-801-368-392	Sequence 392, App
27	76.5	7.0	254	US-10-080-644-5	Sequence 5, Appl1
28	76.5	7.0	372	US-09-813-408-9	Sequence 9, Appl1
29	76	7.0	275	US-08-322-678-8	Sequence 8, Appl1
30	76	7.0	275	US-09-813-408-18	Sequence 18, Appl1
31	76	7.0	275	US-10-033-325-4	Sequence 4, Appl1
32	76	7.0	275	US-09-060-854B-4	Sequence 4, Appl1
33	76	7.0	280	US-09-731-872-314	Sequence 14, App
34	76	7.0	357	US-09-837-235-15	Sequence 15, Appl1
35	76	7.0	434	US-09-971-536-62	Sequence 62, Appl1
36	75.5	6.9	380	US-09-813-408-16	Sequence 16, Appl1
37	75	6.9	297	US-10-080-644-7	Sequence 7, Appl1
38	75	6.9	535	US-09-995-749A-13	Sequence 13, Appl1
39	75	6.9	1781	US-09-995-749A-2	Sequence 2, Appl1
40	74.5	6.8	274	US-08-322-678-9	Sequence 9, Appl1
41	74.5	6.8	274	US-09-813-408-17	Sequence 17, Appl1
42	74.5	6.8	274	US-10-033-325-5	Sequence 5, Appl1
43	74.5	6.8	274	US-09-060-854B-5	Sequence 5, Appl1
44	74.5	6.8	363	US-09-797-464A-11	Sequence 11, Appl1
45	74	6.8	184	US-09-734-017A-78	Sequence 78, Appl1

ALIGNMENTS

RESULT 1

US-10-028-247-4

Sequence 4, Application US/10028247

Patent No. US20020150594A1

GENERAL INFORMATION:

APPLICANT: Goldman, Stanley

APPLICANT: Lathrop, Stephanie J.

APPLICANT: Longchamp, Pascal F.

APPLICANT: Whalen, Robert G.

APPLICANT: Maxygen, Inc.

TITLE OF INVENTION: Methods and Compositions for Developing Spore Display

FILE REFERENCE: 18097A-033520US

CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: US/10/028,247

PRIOR FILING DATE: 2000-06-26

PRIOR APPLICATION NUMBER: US 60/214,161

PRIOR FILING DATE: 2001-06-26

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4

LENGTH: 212

TYPE: PRT

ORGANISM: Bacillus circulans

FEATURE:

OTHER INFORMATION: lipase 396

US-10-028-247-4

Query Match

Best Local Similarity 97.6%

Matches 207; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Query 1 MKFVKRRRIALVTILVSVTSLFAMOPSAKAEHNPVYVHGIGASTNFGISYLSQ 60

Db 1 MKFVKRRRIALVTILVSVTSLFAMOPSAKAEHNPVYVHGIGASTNFGISYLSQ 60

QY 61 GMSRGKLYAVDFMDKGTGNNYNGPVLSFEYQKVDLDEGAKKVDIVAHSMGANTPYIKN 120

Db 61 GMSRGKLYAVDFMDKGTGNNYNGPVLSFEYQKVDLDEGAKKVDIVAHSMGANTLYIKN 120

QY 121 LDGNGKIENVVTLGAGNRSTTSKALPGTDPNOKILYTSYSSADMIYVNYLSKIDGAKNA 180

```
Db 121 LDGSKNLENNVTGGANRLTTSKALPCTDPNOKLLYSITSADMIYMLSKLDGAKNV 180
QY 181 QHGVGHIGLMSQVNSLIKEGLNGGONTN 212
Db 181 QHGVGHIGLMSQVNSLIKEGLNGGONTN 212
```

RESULT 2

```
US-09-738-626-3593
; Sequence 3593, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 3593
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3593
```

```
Query Match 14.3%; Score 156; DB 9; Length 324;
Best Local Similarity 32.7%; Pred. No. 1.9e-07;
Matches 35; Conservative 25; Mismatches 43; Indels 4; Gaps 2;
```

```
QY 36 PYVAVHIGGASYNFAGIKSYLSQGSRGKLYAVDFWDMK-TGTYNNNGPVLSEFVQKVL 94
Db 91 PYVAVHIGGASYNFAGIKSYLSQGSRGKLYAVDFWDMK-TGTYNNNGPVLSEFVQKVL 147
QY 95 DETGAKKVDIVAHSMGANTPYIKNLDGKNKIENVTGLGANRST 141
Db 148 LATGASKVIYVGHSGGVLLRYMRYVLAGASKVKHMYSLAVPNHGT 194
```

RESULT 3

```
US-09-738-626-3594
; Sequence 3594, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; CURRENT FILING DATE: 2000-12-18
```

```
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 3594
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3594
```

```
Query Match 11.9%; Score 130; DB 9; Length 300;
Best Local Similarity 24.4%; Pred. No. 6.4e-05;
Matches 33; Conservative 33; Mismatches 47; Indels 22; Gaps 5;
```

```
QY 36 PYVAVHIGGASYNFAGIKSYLSQGSRGKLYAVDFWDMKTGTNNNGPY-----LSRF 89
Db 72 PYVAVHIGGASYNFAGIKSYLSQGSRGKLYAVDFWDMKTGTNNNGPY-----LSRF 123
QY 90 VOKVDETGAKKVDIVAHSMGANTPYIKNLDGKNKIENVTGLGANRST-----T 141
Db 124 IDAVLVLTGAQAQIVLVHSGGVVARYMRTYGGYMKVRHMISITPNHGTLMGILNPM 183
QY 142 SKALPGTDPNOKILY 156
Db 184 TKVSGEGTEKILMH 198
```

RESULT 4

```
US-10-147-467-2
; Sequence 2, Application US/10147467
; Publication No. US20030027295A1
; GENERAL INFORMATION:
; APPLICANT: TAKESHI, Isbii
; APPLICANT: SATOSHI, Mitsuda
; TITLE OF INVENTION: ESTERASE GENE AND ITS USE
; FILE REFERENCE: 20-4336P
; CURRENT APPLICATION NUMBER: US/10/147,467
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Burkholderia cepacia
US-10-147-467-2
```

```
Query Match 11.3%; Score 123; DB 9; Length 363;
Best Local Similarity 27.0%; Pred. No. 0.0004;
Matches 43; Conservative 27; Mismatches 59; Indels 30; Gaps 9;
```

```
QY 13 TIVLVSTSLFAMOPSAK-----AAEHPVAVVHIGGASYNFAGIKSYLSQGSRSR--- 64
Db 26 TVLAMSLAGAQAASATTAVDYAATRYPIIVHGLGTD-KYGGVVEY-----WRIPE 79
QY 65 -----GKLYAVD---FWDMKTGTNNNGPVLSEFVQKVDGAKKVDIVAHSMGANTP 115
Db 80 DLRAHGAAYVAVNLGSGFSDGPY-GRGEOLLAFFVKQVLAATGAOKVNLIGHSGGL-TS 137
QY 116 YIKNLDGKNKIENVTGLG---GANRSTSKALPGTDP 150
Db 138 RYVASV-APELVAVSTTISTPWHGSGPADFVQDLQTD 175
```

RESULT 5

```
US-10-080-644-6
; Sequence 6, Application US/10080644
; Patent No. US20020137172A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria, Alexandra et al.
```

Query Match	8.5%	Score 92.5;	DB 10;	Length 1062;
Best Local Similarity	25.38;	Pred. No. 1.8;		
Matches 60;	Conservative 22;	Mismatches 78;	Indels 77;	Gaps 12;
3 EVKRRITALLV---TILVLSVTSLEFAMQSSAKAAEHNPPVVMHGTGCGASYNFAGRTS----- 55				
I::I::I::I::	I::	I::I::I::	I::I::	I::I::

RESULT 8
US-09-815-242-11886
Sequence 11886, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsem, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: EDITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578

```

; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11886
; LENGTH: 311
; TYPE: PRF
; ORGANISM: Pseudomonas aeruginosa
US-09-913-242-11886
```

```

Query Match
Best Local Similarity 8.1%; Score 88; DB 10; Length 311;
Matches 32; Conservative 19; Mismatches 46; Indels 14; Gaps 5;
```

```

QY 15 LVLSVTSLEA---MPSAKAAEHNPVYVHG-----TGCASYNFAGIKSYLVSGWSRG 65
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 11 LAIGLASLASPLIOASTYQTKYPIVLAHGMGFEDNIIIGVDWF-GIPSLRRDG---A 66

QY 66 KLVAVDEMDKTGTNNYNGPVLSRFVOKVLDGTGAKKVDIVAHSMGANTPY 116
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 67 QVYVTEV-SQLDTSSEVNGEQLLOQVEIVALSQPKYVNLIGHSGFTIRX 116
```

```

RESULT 9
US-09-912-020-281
; Sequence 281, Application US/09912020
; Patent No. US20020045592A1
; GENERAL INFORMATION:
; APPLICANT: Zyskind, Judith
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Forsyth, John
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Froelich, Jamie M.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
; TITLE OF INVENTION: ESCHERICHIA COLI
; FILE REFERENCE: ELITRA.001DV1
; CURRENT APPLICATION NUMBER: US/09/912.020
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: 09/492,709
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/117,405
; PRIOR FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 485
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 281
; LENGTH: 464
; TYPE: PRF
; ORGANISM: E. Coli
US-09-912-020-281
```

```

Query Match
Best Local Similarity 8.0%; Score 87.5; DB 10; Length 464;
Matches 36; Conservative 22; Mismatches 61; Indels 23; Gaps 5;
```

```

QY 58 VSGWSGKGLYAVDEMDKTGT-NTNNGPVLSRFVOKVLD-ETGAKKVDIVAHSMGANTP 115
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 297 VVOAOKAKGKPLVYEAQWDRSTKSLSEGTLLS--LDNQIDATTTGIRKARFNODDALFP 354

QY 116 YYIKN-----LDGKNTENVVTLGCANRSTSKALPGDPMOKILYT 157
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 355 NQVYNAAMLVDTEONAVVITPAALOMGNEGHFVAVLSENKVKSHLVTPGIODSQKVIR 414

QY 158 SIYSSADMIYNYLSKL-DGAK 178
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 415 AGISAGDRVVTGIDRLTEGAK 436
```

```

RESULT 10
US-10-098-174-1
; Sequence 1, Application US/10098174
; Patent No. US20020169288A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: BOWDEN, Maria
; TITLE OF INVENTION: COLLAGEN-BINDING ADHESIN FROM STAPHYLOCOCCUS EPIDERMIDIS.
; FILE REFERENCE: P07136US01/BAS
; CURRENT APPLICATION NUMBER: US/10/098,174
; CURRENT FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: 60/275,718
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 518
; TYPE: PRF
; ORGANISM: Staphylococcus epidermidis
US-10-098-174-1
```

```

Query Match
Best Local Similarity 8.0%; Score 87; DB 9; Length 518;
Matches 47; Conservative 24; Mismatches 63; Indels 86; Gaps 11;
```

```

QY 26 QPSAKAAEHNPVYVHGI-----TGCASYNFAGIKSYLVSGWSRGKL 67
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 94 QLTAAQAKYKNQYVYFVHGVGLVGEDAFSMYPNMGSTKYN--VKQELTKIGRYVHEA 150

QY 68 YAVDFMDKTGTNNYNGPVLSRFVOKVLDGTGAKKVDIVAHSMGANTPY 116
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 151 NGAFA---SSNDYRAVELYYIKGRVDYGAHAANKYGHKRYRYEGIMPDPGPKTI 206

QY 103 DIVAHSMGANTPYIKN-----LDGK--NKIENVVTLGCANR 138
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 207 HLYGHSMGOTIRLMEHFLNGNDEIDYOROGYSDLPFGQGDNMVSTITTLTGPHN 266

QY 139 STTSKALPGTDPNOKILYTSIYSSADMIYNYLSKL-DGAK 178
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 267 GT-----PAAD--KLGSTKFIKD---TINRIGKIGGTR 294
```

```

RESULT 11
US-10-080-644-2
; Sequence 2, Application US/10080644
; Patent No. US20020137172A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria, Alexandra et al.
; TITLE OF INVENTION: 33167, A NOVEL HUMAN HYDROLASE AND USES THEREFOR
; FILE REFERENCE: MNT-140
; CURRENT APPLICATION NUMBER: US/10/080,644
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 09/584,568
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 315
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-080-644-2
```

```

Query Match
Best Local Similarity 8.0%; Score 86.5; DB 12; Length 315;
Matches 25; Conservative 13; Mismatches 30; Indels 15; Gaps 3;
```

```

QY 37 VVMVHIGASYNFAGIKSYLVSGWSRGKLYAVDEMDKTGTNNYNGP-----VLSR 88
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 69 VVFLHGLFGSKTNFNSIAKILAOOTGRR--VLTVD-----ARHHGSPHSPDMSYEIMSQ 121

QY 89 FVQKVLDETGAKKVDIVAHSMG 111
```


Db 122 DLQDLPLPOLGLVPCVVGSHSMG 144

RESULT 12

US-09-815-242-5841

; Sequence 5841, Application US/09815242

; Patent No. US20020061569A1

; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Karl L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trivick, John D.

; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.

; TITLE OF INVENTION: Identification of Essential Genes in

; FILE REFERENCE: ELITRA.011a

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: US/09/815,242

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5841

; LENGTH: 690

; TYPE: PR

; ORGANISM: Staphylococcus aureus

US-09-815-242-5841

Query Match 8.0%; Score 86.5; DB 10; Length 690;
Best Local Similarity 24.1%; Pred. No. 3.8;
Matches 48; Conservative 23; Mismatches 55; Indels 73; Gaps 9;

QY 36 PYVMVHGIGG-----AST-NEAIGKSYLV-----SQGWSRGKLYAVDFMDKTGTNNYN 82

DB 306 PYVEFHGFLGVDNAPALYPNMGCKFKVIELRKQGYNVHQAASVAF---GSNYDR 361

QY 83 GPVLSFVQKVIDETGA-----KKVDIVAHSMGCANTPPY 117

DB 362 AVELYIYIGGVYDAHAHAATYGHRYGTYGIMPNEPGKVVHLVGHSMGQGTIRLM 421

QY 118 IKNLDCGNRIE-----NVVTLGGANR---STTSKALP-----GTDPNQ 152

DB 422 EEFRLRNGNEELAYHKAHGEISPLFTGGHNNVVASITTLATPHNGSQADKFCNTEAVR 481

QY 153 KILYT-----STYSSADM 165

DB 482 KIMFALNRFMGKXSNIDL 500

RESULT 13

US-10-027-805-35

; Sequence 35, Application US/10027805

; Patent No. US20020164725A1

; GENERAL INFORMATION:

; APPLICANT: ROBERTSON, Daniel E.

; MURPHY, Dennis

; REID, John

MAFFIA, Anthony

LINK, Steven

SWANSON, Ronald V.

WARREN, Patrick V.

KOSMOTKA, Anna

TITLE OF INVENTION: ESTERASES

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: FISH & RICHARDSON P.C.

STREET: 4225 EXECUTIVE SQUARE, STE 1400

CITY: LA JOLLA

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/027,805

FILING DATE: 21-Dec-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/602,359

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: HAILE, LISA A.

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 09010/010001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-678-5070

TELEFAX: 619-678-5099

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 262 AMINO ACIDS

TYPE: AMINO ACID

TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN

SEQUENCE DESCRIPTION: SEQ ID NO: 35:

US-10-027-805-35

Query Match 7.8%; Score 85; DB 9; Length 262;
Best Local Similarity 25.2%; Pred. No. 1.5;
Matches 40; Conservative 23; Mismatches 62; Indels 34; Gaps 8;

QY 36 PYVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVD-----FMDKTGTNNNGPV---LS 87

DB 22 PIVFVHG-WTANNF-----WKQRRYFAGRNMMLFVDNRGHRSDRPLGYDFY 69

QY 88 RF-----VQKVIDETGAKKVDIVAHSMGCANTPPYIKNLDCGNKIENVVTLGGANRSTT 141

DB 70 RFENFISDLDAYVREVEFEVLYVGHSGFMISMKICS--EYNNRYLALILIGGSRILK 127

QY 142 SKALPCTDPNOKILTYSTIYSSADMIVANVLSKLDGAKNA 180

DB 128 LHRI--GYPLAKILIASIAVKKSSRLV---ADLSPFKNA 160

RESULT 14

US-10-027-804-35

; Sequence 35, Application US/10027804

; Publication No. US20030054530A1

; GENERAL INFORMATION:

; APPLICANT: ROBERTSON, Daniel E.

; MURPHY, Dennis

; REID, John

; MAFFIA, Anthony

; LINK, Steven

; SWANSON, Ronald V.

; WARREN, Patrick V.

; KOSMOTKA, Anna

; TITLE OF INVENTION: ESTERASES

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 16:19:36 ; Search time 20 Seconds
(without alignments)
1019.025 Million cell updates/sec

Title: US-09-905-666a-55

Perfect score: 1088

Sequence: 1 MKFVKRRITIALVTILVLSVT.....NSQVNSLKEGLNGGQNTN 212

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1020	93.8	212	2 S23934	lipase lipA - Bac
2	731.5	67.2	210	2 C69652	probable lipase -
3	208	19.1	237	2 G75316	probable lipase -
4	178	16.4	290	2 T36757	probable secreted
5	153.5	14.1	202	2 S77556	hypothetical prote
6	149	13.7	286	2 T26657	hypothetical prote
7	145	13.3	211	2 AE1975	hypothetical prote
8	142.5	13.1	344	2 T27932	hypothetical prote
9	139.5	12.8	300	2 T20712	hypothetical prote
10	139.5	12.8	358	1 A48952	triacylglycerol li
11	137.5	12.6	371	2 T24853	hypothetical prote
12	137.5	12.1	474	2 B64700	lipase homolog - A
13	131	12.0	292	2 T33322	hypothetical prote
14	130	11.9	364	1 A39133	triacylglycerol li
15	130	11.9	479	2 A97027	hydrolyase of alpha
16	129	11.9	300	2 AD1551	hypothetical prote
17	124.5	11.4	171	2 S15911	hypothetical prote
18	124.5	11.4	339	2 C82486	lactonizing lipase
19	123.5	11.4	329	2 T24285	hypothetical prote
20	122	11.2	364	1 J70579	triacylglycerol li
21	121	11.1	323	2 S61927	lipase A precursor
22	121	11.1	333	2 T23227	hypothetical prote
23	119	10.9	340	2 T31812	hypothetical prote
24	115.5	10.6	335	2 T18906	hypothetical prote
25	115	10.6	309	2 G83044	lipase LipC PA4813
26	111	10.2	488	2 A95301	hypothetical prote
27	109	10.0	281	2 T20894	hypothetical prote
28	107	9.8	277	2 T32460	hypothetical prote
29	106	9.7	497	2 H83886	hypothetical prote

30	104.5	9.6	299	2 AF1193	hypothetical prote
31	103.5	9.5	237	2 T26660	hypothetical prote
32	101.5	9.3	299	2 T23932	hypothetical prote
33	100.5	9.2	681	2 G90075	triacylglycerol li
34	97.5	9.0	268	2 S73694	triacylglycerol li
35	97.5	9.0	1519	2 S41525	major ring-forming
36	96.5	8.9	1335	2 T17508	glycoprotein Vp260
37	96	8.8	377	2 A82713	triacylglycerol li
38	94.5	8.7	438	2 B83295	hypothetical prote
39	94	8.6	267	2 F90516	esterase/lipase 1
40	94	8.6	688	2 A47705	triacylglycerol li
41	93.5	8.6	272	2 E97008	periplasmic amino
42	93.5	8.6	638	2 AH0340	putative autotransp
43	93	8.5	682	2 S68970	triacylglycerol li
44	92.5	8.5	1062	2 F83335	RND multidrug effl
45	92.5	8.5	1062	2 T30830	hypothetical prote

ALIGNMENTS

RESULT 1

S23934
lipase lipA - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 15-Oct-1999
C:Accession: S23934; B69652
R:Darbois, V., Baulard, A., Schanck, K., Colson, C.
Biochim. Biophys. Acta 131, 253-260, 1992
A:Title: Cloning, nucleotide sequence and expression in Escherichia coli of a lipase
A:Reference number: S23934; MUID:92329538; PMID:1320940
A:Accession: S23934
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-212 <DAR>
A:Cross-references: GB:M74010; MID:9143153; PIDN:AAA22574.1; PID:9143154
R:Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C:Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capiano, V.; Carter, N.M.;
A.: Enllich, S.D.; Emerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrati,
Mature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
leeh, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holseppel, S.; Hosono, S.; Hullo, M
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y, M.; Oawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scani
A:Authors: Schleich, S.; Schroeter, R.; Scorfione, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Togonoh, A.; Tosato, V.; Uchida
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the gram-positive bacterium Bacillus subtilis
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: B69652
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-132, 'L', 134-212 <RUN>
A:Cross-references: GB:Z99105; GB:AL009126; MID:92632457; PIDN:CAB12064.1; PID:el1822
A:Experimental source: strain 168
C:Genetics:
A:Gene: lipA

Query Match 93.8%; Score 1020; DB 2; Length 212;
Best local similarity 92.9%; Pred. No. 1.8e-77;

Matches 197; Conservative 8; Mismatches 7; Indels 0; Gaps 0.

QY	1	MKFVKRRITIALVTILVLSVTSLPAMQPSAKAAEHNPVWVHGIGASVYFAGIKSYLSQ	60
DB	1	MKFVKRRITIALVTILVLSVTSLPALQPSAKAAEHNPVWVHGIGASVYFAGIKSYLSQ	60
QY	61	GMSRGLVAVDPMKGTGTNYNNGPVLSRPVQVLDLGTGKKYDIYVAHSGGANTPYTKN	120
DB	61	GMSRGLVAVDPMKGTGTNYNNGPVLSRPVQVLDLGTGKKYDIYVAHSGGANTPYTKN	120

C:Species: *Synechocystis* sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

C:Accession: S77556

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M. Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S77556

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-202 <KAN>

A:Cross-references: EMBL:D90905; GB:AB001339; NID:g1652360; PIDN:BA17403.1; PID:d101813

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Genetics:

A:Start codon: GTG

Query Match 14.1%; Score 153.5; DB 2; Length 202;

Best Local Similarity 30.7%; Pred. No. 1.5e-05;

Matches 35; Conservative 27; Mismatches 45; Indels 7; Gaps 3;

QY 29 AKAENPVVHVGIGASYNFAGIKSYLVSGMSRGLYAVDFMDKTGTNNNGPYLSR 88

DB 3 AEPDRHPPVLYVHIGYDTRAKFATWDFLTKGMS--VHCLDLVPNDGS--TSLALLAE 57

QY 89 FVQKVLDEFGA--KQVDYVAHSMGANTPYIKNLGDKNIENVVTLGGANRST 140

DB 58 QVQYIDOKFAPQDPVLDIGFSMGLVTRYIQLGGEHVRRTYITISAPNOGT 111

RESULT 6

T26657

hypothetical protein Y38E10A.g - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T26657

R:Wallis, J.

A:Reference number: Z20252

A:Accession: T26657

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-286 <WIL>

A:Cross-references: EMBL:AL110484; PIDN:CA854398.1; CESP:Y38E10A.g

A:Experimental source: clone Y38E10A

C:Genetics:

A:Gene: CESP:Y38E10A.g

A:Introns: 63/2; 221/2; 261/3

C:Superfamily: *Caenorhabditis elegans* hypothetical protein C09E8.2

Query Match 13.7%; Score 149; DB 2; Length 286;

Best Local Similarity 26.1%; Pred. No. 5.7e-05;

Matches 55; Conservative 30; Mismatches 71; Indels 55; Gaps 8;

QY 36 PVMVHVGIGASYNFAGIKSYLVSGMSRGLYAVDFMDKTGTNNNGPYLSRFYQV-- 93

DB 66 PVLVHGTNSAGTFAPQAYFRANQSEETVYATITGACGYTANVKKLCYQOIRN 125

QY 94 ----LDEGAKKVDYVAHSMGANTPYIKNLGDKNIENVVTLG-----G 135

DB 126 MIAVNAFTQOKVNVIGYSMG--SPIARKAILGKCAEYVQLGAPLTSIIETYSVAG 182

QY 136 ANRST-----TSKALPG-----TDPNOKLTY-----SYSSAD----- 164

DB 183 ANNGTLCIDILRAPLVVPCNTKNGKCSDFLTDIRSVSAVEGQYIFSTIGSPDKVGF 242

QY 165 MIWNYLSKLDGAKNAQIHGVG--HIGLLMNS 194

DB 243 NIVCGRVSRIIDGATAEKDNVPGNHDAIANT 273

RESULT 7

AE1975

hypothetical protein alr1352 [imported] - *Nostoc* sp. (strain PCC 7120)

C:Species: *Nostoc* sp.

A:Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002

C:Accession: AE1975

R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kunitz, T.; Sasamoto, S.; Watanabe, A.; Irtigu

Nakazaki, M.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AE1975

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-211 <KUR>

A:Cross-references: GB:BA000019; PIDN:BA873309.1; PID:g17130699; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr1352

Query Match 13.3%; Score 145; DB 2; Length 211;

Best Local Similarity 26.5%; Pred. No. 8.3e-05;

Matches 54; Conservative 33; Mismatches 77; Indels 40; Gaps 8;

QY 33 EHNPPVHVGIGASYNFAGIKSYLVSGMSRGLYAVDFMDKTGTNNNGPY--LSRFVQ 91

DB 7 QRRPVLLVHIGITTEVEFVFNMAVYLRQLGNTVTLVLP-----NNGEAPLVNLAQ 57

QY 92 KVLDE-----TGAKKVDYVAHSMGANTPYIKNLGDKNIENVVTLGGANRST--SK 143

DB 58 QVADVYCATITTPQPPDLVGFSGIVSRYYQKLGISRVQFVYISSPHHGTVAAYS 117

QY 144 ALPG-----TDPN-----QKLYTSYSSAD--MIWNYLSKLDGAKNAQIHGV 185

DB 118 QHPCVQMRPNSLFLDLNBDVQMLEQNLFTSIWTFYDLMIITPHSSKMPVGEKELPIVA 177

QY 186 GHIGLMMN-----SOVNSLKEGLN 205

DB 178 LHSMLKDKPRSTFVAVAAALAEPIIN 201

RESULT 8

T27932

hypothetical protein ZK617.2 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T27932

R:White, S.

A:Reference number: Z20442

A:Accession: T27932

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-344 <WIL>

A:Cross-references: EMBL:Z73897; PIDN:CA98062.1; GSPDB:GN00022; CESP:ZK617.2

A:Experimental source: clone ZK617

C:Genetics:

A:Gene: CESP:ZK617.2

A:Introns: 62/2; 121/3; 288/2

A:Map position: 4

Query Match 13.1%; Score 142.5; DB 2; Length 344;

Best Local Similarity 26.0%; Pred. No. 0.00025;

Matches 53; Conservative 29; Mismatches 65; Indels 57; Gaps 9;

QY 36 PVMVHVGIGASYNFAGIKSYLVSGMSRGLYAVDFMDKTGTNNNGPYLS----- 87

DB 65 PVEFVHGLNNEAGSLWKIARDFTNANVPROYLFPAT--WGKGTEPLMLNVAMSCSTHYQHR 123

QY 88 RFVQKVLDEFGAKKVDYVAHSMGANTPYIKNLGDKNIENVVTLGGANRST--VVT 132

DB 124 RFETVLKTYGAKQIDVIGYSMG--SPIARKAILGKCAVDNPNVALGPSLHSRVHTYS 180

Mon May 19 10:47:10 2003

us-09-905-666a-55.rpr

Page 6

```

QY      151 NOKILYTSIYSSADMIYVNLKLDGAKNAQIHGVC-HIGLMSQVNSLIKE 202
      ::      ||      | | | |      : | : | : |
Db      338 DK-----IYRAVSNFPDKYY-KILGDKNPDFYTAARQFSTYSSSKFNEVKD 383

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Search completed: May 9, 2003, 16:22:24
Job time : 23 secs
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GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 16:17:45 ; Search time 12 Seconds
(Without alignments)
.732.748 Million cell updates/sec

Title: US-09-905-666a-55

Perfect score: 1088
Sequence: 1 MKFVKRRILALVTIIVLSVT.....NSQVNSLKEGLNGGCONTN 212

Scoring table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt.40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1023	94.0	212	1	LIP_BACSU
2	139.5	12.8	358	1	LIP_PSEGL
3	125	11.5	364	1	LIP_BURCE
4	124.5	11.4	312	1	LIP_VIRCH
5	122	11.2	364	1	LIP_PSESS
6	97.5	9.0	268	1	ESL2_MYCPN
7	94	8.6	688	1	LIP_STARP
8	88.5	8.1	373	1	ACOC_ALCEU
9	88	8.1	311	1	LIP_PSEAB
10	88	8.1	311	1	LIP_PSEAB
11	87.5	8.0	415	1	YEGM_ECOLI
12	87.5	8.0	485	1	Y045_MYCPN
13	87	8.0	1953	1	BNIL_YEAST
14	86.5	8.0	277	1	LIP_PSEER
15	86.5	8.0	293	1	MHPQ_ECOLI
16	86.5	8.0	690	1	LIP_STAAU
17	86	7.9	719	1	CLIA_BACTK
18	85	7.8	719	1	CLID_BACNU
19	85	7.8	1023	1	HEX1_ECOLI
20	85	7.8	1052	1	RH32_ACTPL
21	84	7.7	619	1	CHIT_STRII
22	83.5	7.7	213	1	XYNA_BACCI
23	83.5	7.7	456	1	ENO_MYCPV
24	83	7.6	501	1	TACY_PAEAL
25	82.5	7.6	268	1	ESL2_MYCGE
26	82	7.5	358	1	ALF_BUCAL
27	82	7.5	358	1	ALF_BUCAL
28	82	7.5	1266	1	ALYS_ENTFA
29	81.5	7.5	213	1	AIDA_ECOLI
30	81.5	7.5	351	1	XYNA_BACSU
31	81.5	7.5	623	1	ADH_CLOBE
32	81	7.4	326	1	PDAT_SCHPO
33	81	7.4	372	1	TGL2_YEAST
					FLGI_BUCAT

34	81	7.4	662	1	YME1_SCHMA	P46508 schistosoma
35	81	7.4	684	1	FLID_HELPJ	G92191 helicobacte
36	80	7.4	288	1	PIP_BACCO	P46541 bacillus co
37	80	7.4	350	1	GALE_DROME	G94055 drosophila
38	80	7.4	381	1	SUBN_BACNA	P35835 bacillus su
39	80	7.4	427	1	TOLB_HAELN	P44677 haemophilus
40	80	7.4	587	1	YS48_CAEEL	G09374 caenorhabdi
41	80	7.4	684	1	FLID_HELPY	P67866 helicobacte
42	79.5	7.3	274	1	SUBD_BACCI	P00781 bacillus li
43	79.5	7.3	288	1	YI34_MYCTU	G50599 mycobacteri
44	79	7.3	514	1	TUBE_DROVI	G08171 drosophila
45	79	7.3	546	1	AMYB_BACCE	P36924 bacillus ce

ALIGNMENTS

RESULT 1	ID	Sequence	Score	Length	Start	End	Frame	Database	Description
LIP_BACSU	AC	P37957: 034644:	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	DT	01-OCT-1994 (Rel. 30, Created)	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	DT	30-MAY-2000 (Rel. 39, Last sequence update)	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	DT	15-JUN-2002 (Rel. 41, Last annotation update)	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	DE	Lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	GN	LIPASE OR LIP.	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	OS	Bacillus subtilis.	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	OX	NCBI_TaxID=1423;	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RP	SEQUENCE FROM N.A.	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RC	STRAIN=168;	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RX	MEDLINE=92329538; PubMed=1320940;	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	Dartois V., Baulard A., Schanck K., Colson C.;	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	"Cloning, nucleotide sequence and expression in Escherichia coli of a	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	lipase gene from Bacillus subtilis 168."	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	Biochim. Biophys. Acta 1131:253-260(1992).	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RP	SEQUENCE FROM N.A.	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RC	STRAIN=168;	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RX	MEDLINE=98044033; PubMed=9384377;	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	Azevedo V., Bertero M.C., Bessieres P., Bojotin A., Borchert S.,	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	Choi S.K., Codan J.J., Conerton I.F., Cummings N.J., Carter R.A.,	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	Enlian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	Fritz C., Glaser P., Goffeau A., Golightly E.J., Grandi G.,	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	Hilbert H., Holstappel S., Hosono S., Hullio M.F., Itaya M., Jones L.,	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	Joris B., Karamella D., Kasahara Y., Klatier Blanchard M., Klein C.,	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	Kobayashi Y., Koeltter P., Koningsstein G., Krogh S., Kumano M.,	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	Kunita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	Medina N., Meliando R.P., Mizuno M., Moesti D., Nakai S., Noback M.,	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	Paro V., Pohl T.M., Portetelle D., Portoullik S., Prescott A.M.,	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	Pressecen E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	Sorokin A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,	1023	212	1	212	AA	STANDARD	LIP_BACSU
LIP_BACSU	RT	Takeuchi M., Tamakoshi A., Tanaka T., Terpilstra P., Tognoni A.,	1023	212	1	212	AA	STANDARD	LIP_BACSU

RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viaril A., Wambuit R., Wedler E., Wedler H., Weitzengger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danphin A.;
 RT "the complete genome sequence of the Gram-positive bacterium *Bacillus*
 RT *subtilis*,"
 RL Nature 390:249-256(1997).
 CC -1- CATALYTIC ACTIVITY: triacylglycerol + H(2)O = diacylglycerol + a
 CC fatty acid anion.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -----
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 CC -----
 CC EMBL: M74010; AAA22574.1; -
 CC EMBL: AB000617; BAA2231.1; -
 CC EMBL: 299105; CAB12064.1; -
 CC PIR: S23934; S23934.
 CC Subtilisin: BG10679; 1lpa.
 CC InterPro: IPR002918; Lipase_2.
 CC InterPro: IPR000379; Ser_estrs.site.
 CC DR Pfam: PF01674; Lipase_2; 1.
 CC DR Hydrolyase: Lipid degradation; Signal; Complete proteome.
 CC FT SIGNAL. 1 24
 CC FT CHAIN 25 212 LIPASE.
 CC FT ACT_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT CONFLICT 133 133 L -> V (IN REF. 1).
 CC FT SEQUENCE 212 AA; 22791 MW; B6A70E02746118BF CRC64;
 CC
 CC Query Match 94.0%; Score 1023; DB 1; Length 212;
 CC Best Local Similarity 93.4%; Pred. No. 4; 1e-79;
 CC Matches 199; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
 CC
 CC QY 1 MKPKRRIILVLTIVSVSLFAPSARAAENPVVWVHGICGASTYRAGISYLSQ 60
 CC DB 1 MKPKRRIILVLTIVSVSLFAPSARAAENPVVWVHGICGASTYRAGISYLSQ 60
 CC QY 61 GWSGKRYADEVMDKCTGNTNNGPVLSRFVOKVDETGAKKVDIVANSMGCANPYIKN 120
 CC DB 61 GWSGKRYADEVMDKCTGNTNNGPVLSRFVOKVDETGAKKVDIVANSMGCANPYIKN 120
 CC QY 121 LDGKNKIENVVTLGGANRSTTSKALPCTDPNOKILYTSIYSSADMIYANLTKLDGAKNA 180
 CC DB 121 LDGKNKIENVVTLGGANRSTTSKALPCTDPNOKILYTSIYSSADMIYANLTKLDGAKNA 180
 CC QY 181 QIHGVGHIGILMNSQVNSLIKEGLNGGQNTN 212
 CC DB 181 QIHGVGHIGILYSSQVNSLIKEGLNGGQNTN 212
 CC
 CC RESULT 2
 CC LIP_PSEGL STANDARD: PRT; 358 AA.
 CC ID LIP_PSEGL
 CC AC Q05489;
 CC DT 01-OCT-1994 (Rel. 30, Created)
 CC DT 01-OCT-1994 (Rel. 30, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE Lipase precursor (EC 3.1.1.3) (triacylglycerol lipase).
 CC GN LIPA.
 CC OS Pseudomonas glumae, and
 CC OS Chromobacterium viscosum.
 CC OC Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
 CC OC Burkholderia.
 CC NCBI_TaxID=337, 42739;
 CC RN [1]
 CC RC SEQUENCE FROM N.A., SEQUENCE OF 40-61, AND MUTAGENESIS.
 CC RP SPECIES-E. glumae; STRAIN-PGI / CBS 322.89;
 CC RX MEDLINE=93119130; PubMed=1476423;

RA Frenken L.G.J., Egmond M.R., Batenburg A.M., Bos J.W., Visser C.,
 RA Vlieghe C.T.;
 RT "Cloning of the *Pseudomonas glumae* lipase gene and determination of
 RT the active site residues,"
 RL Appl. Environ. Microbiol. 58:3787-3791(1992).
 CC [2]
 CC SEQUENCE OF 40-54, AND CHARACTERIZATION.
 CC SPECIES-C. viscosum;
 CC MEDLINE=95306500; PubMed=7786905;
 CC RA Taipa M.A., Liberton K., Costa J.V., Cabral J.M.S., Jaeger K.-E.;
 RT "Lipase from *Chromobacterium viscosum*: biochemical characterization
 RT indicating homology to the lipase from *Pseudomonas glumae*,"
 RL Biochim. Biophys. Acta 1256:396-402(1995).
 CC [3]
 CC X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 CC SPECIES-P. glumae;
 CC MEDLINE=94009622; PubMed=8405390;
 CC RA Noble M.E.M., Cleasby A., Johnson L.N., Egmond M.R., Frenken L.G.J.;
 RT "The crystal structure of triacylglycerol lipase from *Pseudomonas*
 RT glumae reveals a partially redundant catalytic aspartate,"
 RL FEBS Lett. 331:123-128(1993).
 CC [4]
 CC X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 CC SPECIES-C. viscosum; STRAIN-ARCC 6918;
 CC MEDLINE=96275656; PubMed=8683577;
 CC RA Lang D., Hofmann B., Haalck L., Hecht H.-J., Spener F., Schmid R.D.,
 RA Schomburg D.;
 RT "Crystal structure of a bacterial lipase from *Chromobacterium*
 RT viscosum ATCC 6918 refined at 1.6-A resolution,"
 RL J. Mol. Biol. 259:704-717(1996).
 CC -1- FUNCTION: HYDROLYSIS OF TRIGLYCERIDES.
 CC -1- CATALYTIC ACTIVITY: triacylglycerol + H(2)O = diacylglycerol + a
 CC fatty acid anion.
 CC -1- COFACTOR: REQUIRES CALCIUM.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY. PSEUDOMONAS
 CC LIPASE FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: X70354; CAA49812.1; -
 CC EMBL: A16323; CAA01279.1; -
 CC DR EMBL: A32021; CAA02073.1; -
 CC DR PIR: A48952; A48952.
 CC DR PIR: S37291; S37291.
 CC DR PDB: 1TAH; 3I-MAY-94.
 CC DR InterPro: IPR000073; Abhydrolase.
 CC DR InterPro: IPR000734; Lipase.
 CC DR InterPro: IPR000379; Ser_estrs.site.
 CC DR Pfam: PF00561; abhydrolase; 1.
 CC DR PROSITE: PS00120; LIPASE_SER; 1.
 CC KM Hydrolyase: Lipid degradation; Signal; Calcium; 3D-structure.
 CC FT SIGNAL. 1 39
 CC FT CHAIN 40 358
 CC FT ACT_SITE 126 126 LIPASE.
 CC FT ACT_SITE 302 302 CHARGE RELAY SYSTEM.
 CC FT ACT_SITE 324 324 CHARGE RELAY SYSTEM.
 CC FT DISULFID 229 308
 CC FT MOTAGEN 54 54
 CC FT MOTAGEN 126 126
 CC FT MOTAGEN 160 160
 CC FT MOTAGEN 160 160
 CC FT MOTAGEN 160 160
 CC FT MOTAGEN 280 280
 CC FT MOTAGEN 280 280
 CC FT MOTAGEN 302 302
 CC
 CC H->A: NO LOSS OF ACTIVITY.
 CC S->A: COMPLETE LOSS OF ACTIVITY.
 CC D->E: NO LOSS OF ACTIVITY.
 CC D->A: NO LOSS OF ACTIVITY.
 CC D->E: NO LOSS OF ACTIVITY.
 CC D->A: COMPLETE LOSS OF ACTIVITY.
 CC D->E: NO LOSS OF ACTIVITY.

FT MUTAGEN 302 302 D->A: 75% LOSS OF ACTIVITY.
 FT MUTAGEN 324 324 H->A: COMPLETE LOSS OF ACTIVITY.
 FT CONFLICT 40 40 A->W (IN REF. 2).
 SQ SEQUENCE 358 AA: 36928 MW: FEI7B5D/AZ2EC6B4B CRC64:

Query Match 12.8%; Score 139.5; DB 1; Length 358;
 Best Local Similarity 29.6%; Pred. No. 0.00014;
 Matches 48; Conservative 26; Mismatches 59; Indels 29; Gaps 8;

OY 1 MKVKRRIIALVILVLSVSL-----FAMPSAKAE-----HNPVWVGIGASY 48
 DB 2 VSRMSRVRARAVAMALVPLAGAGLTMASPAADVATATRYPIVLVHGLAGTD- 60
 OY 49 NFA-----GIKSYLVSGMSRGLAYD---FMDKTGTNNNGPYLSRFVOKVIDETG 98
 DB 61 KFNANVDYMWGIGDLSHSG---AKYVANLSGFSDDGN-GRGEQLLAYVQVLAATG 116
 OY 99 AKKVDIVAHSMGANTPYITKNDGKNLENNVTLCANST 140
 DB 117 ATKVNLIHSGGLTSRYVA--AVAPOLVASVTTIGTPHRGS 156

RESULT 3

LIP_BURCE STANDARD: PRT; 364 AA.

AC P22088;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).
 GN LIP.
 OS Burkholderia cepacia (Pseudomonas cepacia).
 OC Bacteria: Proteobacteria: beta subdivision; Burkholderia group;
 OC Burkholderia.
 OX NCBI_Taxid=292;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 45-66.
 RC STRAIN-DSM 3959;
 RX MEDLINE-91100343; PubMed-1987151;
 RA Joergensen S., Skov K.W., Diderichsen B.;
 RT "Cloning, sequence, and expression of a lipase gene from Pseudomonas
 cepacia: lipase production in heterologous hosts requires two
 pseudomonas genes.";
 RT J. Bacteriol. 173:559-567(1991).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RX MEDLINE-97184684; PubMed-9032073;
 RA Kim K.K., Song H.K., Shin D.H., Hwang K.Y., Suh S.W.;
 RT "The crystal structure of a triacylglycerol lipase from Pseudomonas
 cepacia reveals a highly open conformation in the absence of a bound
 inhibitor.";
 RT Structure 5:173-185(1997).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE-97184685; PubMed-9032074;
 RA Schrag J.D., Li Y., Cygler M., Lang D., Burgdorf T., Hecht H.-J.,
 RA Schmid R., Schomburg D., Rydel T.J., Oliver J.D., Strickland L.C.,
 RA Dunaway C.M., Larson S.B., Day J., McPherson A.O.;
 RT "The open conformation of a Pseudomonas lipase.";
 RT Structure 5:187-202(1997).
 RN [4]
 RP CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
 fatty acid anion.
 CC -1- COFACTOR: REQUIRES CALCIUM.
 CC -1- SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY. PSEUDOMONAS
 LIPASE FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
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CC EMBL: M58494; AAA50466.1; -
 CR PIR: A39133; A39133.
 DR PDB: 1O1L; 15-MAR-97.
 DR PDB: 2LIP; 12-MAR-97.
 DR PDB: 3LIP; 16-JUN-97.
 DR InterPro: IPR000073; Abhydrolase.
 DR InterPro: IPR000734; Lipase.
 DR InterPro: IPR000379; Ser-estrs_site.
 DR Pfam: PF00561; abhydrolase_1.
 DR PROSITE: PS00120; LIPASE_SER; 1.
 KW Hydrolyase; Lipid degradation; Signal; Calcium; 3D-structure.
 FT CHAIN 1 44
 FT SIGNAL 1 44
 FT ACT_SITE 131 131
 FT ACT_SITE 286 286
 FT ACT_SITE 330 330
 SQ SEQUENCE 364 AA: 37494 MW: E9CD2DFB55658E9 CRC64;

Query Match 11.5%; Score 125; DB 1; Length 364;
 Best Local Similarity 28.2%; Pred. No. 0.0024;
 Matches 40; Conservative 27; Mismatches 51; Indels 24; Gaps 8;

OY 14 ILVLSVT--SLFAMPSA-KAENHPVWVHGIGASYNFAGIKSYLVSGM----- 62
 DB 29 VMLTATTHAMAMADPAAGAAATRYPIVLVHGLSGTD-KYAGVLEY-----WVGIGEDLO 82
 OY 63 -SGKGLAYD---FMDKTGTNNNGPYLSRFVOKVIDETGAKKVDIVAHSMGANTPYIT 118
 DB 83 QNCATVYVANLSGFSDDGN-GRGEQLLAYVQVLAATGATRVNLVHSGGLTSRYVA 141
 OY 119 KNDGKNLENNVTLCANST 140
 DB 142 --AVAPDLVASVTTIGTPHRGS 161

RESULT 4

LIP_VIRCH STANDARD: PRT; 312 AA.

AC P15493; O07349; Q9KRM7;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactonizing lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).
 GN LIPA OR HLVC OR VCA0221.
 OS Vibrio cholerae.
 OC Bacteria: Proteobacteria: gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_Taxid=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-El Tor O17 / Serotype O1;
 RX MEDLINE-90286918; PubMed-2162464;
 RA Alm R.A., Manning P.A.;
 RT "Characterization of the hlyB gene and its role in the production of
 the El Tor haemolysin of Vibrio cholerae O1.";
 RT Mol. Microbiol. 4:413-425(1990).
 RN [2]
 RP IDENTIFICATION AND REVISIONS.
 RC STRAIN-El Tor O17 / Serotype O1;
 RA Manning P.A.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-El Tor N16961 / Serotype O1;
 RX MEDLINE-20406833; PubMed-10952301;
 RA Heideberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Uitterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;

```

RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483(2000).
CC -1- FUNCTION: CATALYZES THE SYNTHESIS OF MACROCYCLIC LACTONES IN
CC ANHYDROUS ORGANIC SOLVENTS.
CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -1- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
CC -----
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RL Agric. Biol. Chem. 55:2349-2357(1991).
CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -1- SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY. PSEUDOMONAS
CC LIPASE FAMILY.
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CC -----
 DR EMBL: AE000035; AAB96016.1; -
 DR InterPro: IPR000073; Abhydrolase.
 DR InterPro: IPR000379; Ser-estrs-site.
 DR Pfam: PF00561; abhydrolase_1.
 KM Hypothetical protein; Hydrolase; Serine esterase; Complete proteome.
 FT ACT SITE 28 28
 FT ACT SITE 96 96 CHARGE RELAY SYSTEM (BY SIMILARITY).
 SQ SEQUENCE 268 AA: 30784 MW: 29D5F87E12090C9B CRC64;

Query Match 9.0%; Score 97.5; DB 1; Length 268;
 Best Local Similarity 32.7%; Pred. No. 0.34;
 Matches 32; Conservative 14; Mismatches 39; Indels 13; Gaps 6;

QY 21 SIFAMPSSKAHNPVWVHGIGASYNFAGIKSYLVSGSRGKLVAVDFDKTGY 80
 DB 11 SIFAEPRHRK--RHN-FIFLHGSGSEYSSFKHVFLEKKRMS--FFAFNF-PGHGNNQ 63
 QY 81 NNGP--VLSRFVQKVL D--ETGAKKVDIVAHSMGA 112
 DB 64 SNSVDLKLKHVELVCDFTIOLKRLKKVVLVGHSMGA 101

RESULT 7
 LIP_STAEF STANDARD: PRT; 688 AA.
 ID LIP_STAEF
 AC 002510;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lipase precursor (EC 3.1.1.3) (Glycerol ester hydrolase).
 GN GENC.
 OS Staphylococcus epidermidis.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1282;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 303-315.
 RC STRAIN=9;
 RX MEDLINE=93171870; PubMed=8436947;
 RA Farrell A.M., Foster T.J., Holland K.T.;
 RT "Molecular analysis and expression of the lipase of Staphylococcus
 RT epidermidis";
 RL J. Gen. Microbiol. 139:267-277(1993).
 CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
 CC fatty acid anion.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MISCELLANEOUS: THE EXPRESSION OF STAPHYLOCOCCUS LIPASE IS
 CC NEGATIVELY REGULATED BY BACTERIOPHAGE LYSOGENITATION (LIPASE
 CC CONVERSION).
 CC -1- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
 CC -----
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CC -----
 DR EMBL: M95577; AAA19729.1; -
 DR PIR: A47705; A47705.
 DR InterPro: IPR000734; Lipase.
 DR InterPro: IPR000379; Ser-estrs-site.
 DR TIGRfam: TIGR01168; YSIRK_signal; 1.
 DR PROSITE: PS00120; LIPASE_SER; 1.
 KM Hydrolase; Lipid degradation; Zymogen; Signal.

FT SIGNAL 1 35 POTENTIAL.
 FT PROPEP 36 302 REMOVED IN THE MATURE FORM.
 FT CHAIN 303 688 LIPASE.
 FT ACT_SITE 418 418 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 648 648 CHARGE RELAY SYSTEM (BY SIMILARITY).
 SQ SEQUENCE 688 AA: 77198 MW: 70A92F25834B9E31 CRC64;

Query Match 8.6%; Score 94; DB 1; Length 688;
 Best Local Similarity 19.7%; Pred. No. 2.1;
 Matches 46; Conservative 36; Mismatches 61; Indels 90; Gaps 11;

QY 28 SAKAAEH---NPVWVHGIGASYNFAGIKSYLVSGSRGKLVAVDFDKTGY 71
 DB 301 SAKQKQYKNNDDPIIVHGFNGFTD---INPSVLTWVGDDKNNINQDLEENGEAYEAS 357
 QY 72 FMDKTGTNNNGVLSRFVQKVLDEFGA-----KKVDIYA 106
 DB 358 I-SAFGSNDRAVELYYIKGRVYGAHAAKYGHERYKTEGYVKDKMPQOKIHLVG 416
 QY 107 HSMGKAN-----TPYIKNLDDG--NKIENVYTLGAMR 138
 DB 417 HSMGGTTIOLELLRHGNPEVEYOKNGEISPLX-----QGCHNMVSSITTLGTPIN 472
 QY 139 STTSKALPCTDPNOKILTYSISSADMIYNNYLSKLDGAKNAOI-HGYCHIGL 190
 DB 473 GTHASDLTG--NEAIVROLAYD-----VGKMYGNKDSRVDEGLEHML 513

RESULT 8
 ACOC_ALCEU STANDARD: PRT; 373 AA.
 ID ACOC_ALCEU
 AC P27747;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Dihydrolipoamide acetyltransferase component of acetoacetyl
 DE system (EC 2.3.1.12) (Acetoacetyl dehydrogenase E2 component)
 DE (Fast-migrating protein) (FMP).
 GN ACOC.
 OS Alcaligenes eutrophus (Ralstonia eutropha).
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
 OX Ralstonia.
 OX NCBI_TaxID=510;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-27.
 RC STRAIN=H16 / DSM 428 / ATCC 17699;
 RX MEDLINE=91286190; PubMed=2061286;
 RA Priefer H., Hein S., Kruenger N., Zeh K., Schmidt B., Steinbuechel A.;
 RT "Identification and molecular characterization of the Alcaligenes
 RT eutrophus H16 acetoacetyl transferase involved in acetoacetyl
 RT J. Bacteriol. 173:4056-4071(1991).
 CC -1- FUNCTION: DIHYDROLIPOAMIDE ACETYLTRANSFERASE INVOLVED IN
 CC ACETOIN CATABOLISM.
 CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
 CC acetylhydrolipoamide.
 CC -1- COFACTOR: THE E2 COMPONENT CONTAINS ONE COVALENTLY-BOUND LIPOYL
 CC COFACTOR (PROBABLE).
 CC -1- PATHWAY: Acetoacetyl catabolism.
 CC -1- INDUCTION: BY GROWTH ON ACETOIN.
 CC -1- SIMILARITY: CONTRAINS 1 LIPOYL-BINDING DOMAIN.
 CC -----
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CC -----
 DR EMBL: M66060; AAA1950.1; -
 DR PIR: DA2462; DA2462.
 DR HSP: P20706; 1GHR.
 DR InterPro: IPR003089; AB_hydrolase.

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DR InterPro: IPR000073; Abhydrolase.
DR InterPro: IPR000089; Biotin_lipoyl.
DR InterPro: IPR003016; Lipoyl.
DR InterPro: IPR003079; Ser_estrs_site.
DR Pfam: PF00364; biotin_lipoyl.1.
DR Pfam: PF00561; abhydrolase.1.
DR PRINTS: PR00111; ABHYDROLASE.
DR PROSITE: PS00189; Lipoyl.1.
DR Transferase: Acyltransferase; Lipoyl.
FT BINDING 49 49 0
FT SEQUENCE 373 AA; 38904 MW; 9D5CE1F83E94892F CnC64;

Query Match 8.1%; Score 88.5; DB 1; Length 373;
Best Local Similarity 20.7%; Pred. No. 2.9;
Matches 40; Conservative 36; Mismatches 76; Indels 41; Gaps 8;

QY 37 VMMVHGIGGASVY-----FAGIKSYLVSGWNGKLYAVDFMDKNTNNNGEV 85
DB 137 VLEHFGEGDLDNMLFNLDPADATVVALDLPGHGSSPRL-----AGTTLAQ--- 185
QY 86 LSREYQKVLDETGAARKVDIVAHSMGCAATPYIKMLDGNKLENY-----VTLGANST 140
DB 186 MAGFAARMDEGEIAAHVGVHSGVGAQAQA--VDAPORVLSVALVSPVGFDAVNSG 243
QY 141 TSKALPGTDPPNOKT--LYTSIYSSADMVVMYVLSKLDGAKNAQHGVGHIGLLMSQVNS 198
DB 244 YTEGFVSAQSREELKPVVELLFADAGLVSRMLDDL--LRYKRLDGV-----TEALT 293
QY 199 LIKEGLNGGGONT 211
DB 294 ALGGGLFGGGRS 306

RESULT 9
LIP_PSEAE
ID LIP_PSEAE STANDARD; PRT; 311 AA.
AC P36876;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactonizing lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).
GN LIP OR LIPA OR PA2862.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
CC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAOI;
RX MEDLINE=92381478; PubMed=1512563;
RA Wohlfarth S., Hoesch C., Strunk C., Winkler U.K.;
RT "Molecular genetics of the extracellular lipase of Pseudomonas aeruginosa PAOI."
RT J. Gen. Microbiol. 138:1325-1335(1992).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=TE3285;
RX MEDLINE=92337414; PubMed=1632642;
RA Chhaya-Sioml M., Yoshikawa K., Oshima-Hirayama N., Yamamoto K.,
RA Sogabe Y., Nakatani T., Nishioaka T., Oda J.;
RT "Purification, molecular cloning, and expression of lipase from Pseudomonas aeruginosa."
RT Arch. Biochem. Biophys. 296:505-513(1992).
RN [3]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-57.
RC STRAIN=PAOIR;
RX MEDLINE=92247813; PubMed=1576157;
RA Jaeger K.E., Adrian F.-J., Meyer H.E., Hancock R.E.W., Winkler U.K.;
RT "Extracellular lipase from Pseudomonas aeruginosa is an amphiphilic protein."
RT Biochim. Biophys. Acta 1120:315-321(1992).
RN [4]

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RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAOI;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Huffnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Collier L., Tolerino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Laidig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an opportunistic pathogen."
RT Nature 406:959-964(2000).
RN [5]
RP SEQUENCE OF 28-39.
RC STRAIN=EF2;
RX MEDLINE=92085040; PubMed=1748875;
RA Gilbert E.J., Cornish A., Jones C.W.;
RT "Purification and properties of extracellular lipase from Pseudomonas aeruginosa EF2."
RL J. Gen. Microbiol. 137:2223-2229(1991).
CC -1- FUNCTION: CATALYZES THE SYNTHESIS OF MACROCYCLIC LACTONES IN ANHYDROUS ORGANIC SOLVENTS.
CC -1- CATALYTIC ACTIVITY: triacylglycerol + H(2)O -> diacylglycerol + a fatty acid anion.
CC -1- SUBCELLULAR LOCATION: DURING EARLY STATIONARY GROWTH PHASE ABOUT 10% OF THE ENZYME MOLECULES REMAIN CELL-BOUND WHILE ABOUT 90% ARE RELEASED INTO THE GROWTH MEDIUM.
CC -1- MISCELLANEOUS: LIPASE OF STRAIN EF2 EXHIBITS SOME ESTERASE ACTIVITY, AND SHOWS A MARKED SPECIFICITY OR THE 1,3-OLEYL RESIDUES OF TRIOLEIN.
CC -1- SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY. PSEUDOMONAS LIPASE FAMILY.
CC
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CC
DR EMBL: X63390; CAA4997.1; -
DR EMBL: AB008452; BAA23128.1; -
DR EMBL: AX000441; CAB77076.1; -
DR EMBL: AE004712; AAG06250.1; -
DR PIR: S25768; S25768.
DR PIR: S24160; S24160.
DR HSSP: P22088; 3LIP.
DR InterPro: IPR000073; Abhydrolase.
DR InterPro: IPR000734; Lipase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00561; abhydrolase.1.
DR PROSITE: PS00120; LIPASE_SER; 1.
KW Hydrolase; Lipid degradation; Signal; Complete proteome.
FT SIGNAL 1 26
FT CHAIN 27 311
FT ACT_SITE 108 108
FT ACT_SITE 235 235
FT ACT_SITE 277 277
FT VARIANT 33 33 K -> Q (IN STRAIN EF2).
FT VARIANT 156 156 V -> I (IN STRAIN TE3285).
FT VARIANT 202 202 Q -> H (IN STRAIN TE3285).
FT VARIANT 204 204 I -> V (IN STRAIN TE3285).
FT VARIANT 204 204
FT SEQUENCE 311 AA; 32723 MW; 7DB1ADF27BDE5619 CnC64;

Query Match 8.1%; Score 88; DB 1; Length 311;
Best Local Similarity 28.8%; Pred. No. 2.6;
Matches 32; Conservative 19; Mismatches 46; Indels 14; Gaps 5;

QY 15 LVLSVTSLEFA--MPSAKAAEHNPVWVG-----TGGASYNFAGIKSYLVSGWNGRG 65
DB 11 LAIGLASLAASPLIDASITYTQTKYPIVLAHGLGFDNLTGVYWF-GIPSLARRGG---A 66

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OY 66 KLYAVDFMDKTGTNNNGPVLRSFYOKVLDGTGAKKVDIVAHSMGSGANTPY 116
 DB 67 QYVYVEV-SQLDTSEYRGEOQLQOYVEIYALSGOPKVNLIHSHGSPITRY 116

RESULT 10
 LIP_PSESP STANDARD: PRT: 311 AA.
 AC P26677:
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactonizing lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).
 GN LIP.
 OS Pseudomonas sp. (strain 109).
 OC Bacteria; Proteobacteria.
 OX NCBI_TaxID=306;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-45.
 RX MEDLINE=92011544; PubMed=1917947;
 RA Ihara F., Kageyama Y., Hirata M., Nihira T., Yamada Y.;
 RT "Purification, characterization, and molecular cloning of lactonizing lipase from Pseudomonas species."
 RL J. Biol. Chem. 266:18135-18140(1991).
 CC -1- FUNCTION: CATALYZES THE SYNTHESIS OF MACROCYCLIC LACTONES IN ANHYDROUS ORGANIC SOLVENTS.
 CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a fatty acid anion.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY. PSEUDOMONAS LIPASE FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: D10166; BAA01035.1; -
 DR PIR: A40943; A40943.
 DR HSSP: P22088; 3LIP.
 DR InterPro: IPR000073; Abhydrolase.
 DR InterPro: IPR000734; Lipase.
 DR InterPro: IPR000379; Ser_ests_site.
 DR Pfam: PF00561; abhydrolase_1.
 DR PROSITE: PS00120; LIPASE_SER; 1.
 KW Hydrolase; Lipid degradation; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 311 LACTONIZING LIPASE.
 FT ACT_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 235 235 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 277 277 CHARGE RELAY SYSTEM (BY SIMILARITY).
 SQ SEQUENCE 311 AA; 32737 MW; 27AC2F3DD3B334D1 CRC64;

Query Match 8.1%; Score 88; DB 1; Length 311;
 Best Local Similarity 28.8%; Pred. No. 2.6;
 Matches 32; Conservative 19; Mismatches 46; Indels 14; Gaps 5;
 OY 15 LVLSTVSLFA---MPSAKAEHNPVVMVHG-----IGASYNFAGIKSYLVSGMSG 65
 DB 11 LAIGLASLASPLDQASTYTGRTKPIVLAHGMFGFNDILGVDYWF-GTSSALRRD---A 66
 OY 66 KLYAVDFMDKTGTNNNGPVLRSFYOKVLDGTGAKKVDIVAHSMGSGANTPY 116
 DB 67 QYVYVEV-SQLDTSEYRGEOQLQOYVEIYALSGOPKVNLIHSHGSPITRY 116

RESULT 11
 YEGM_ECOLI STANDARD: PRT: 415 AA.

AC P76397;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein yegm precursor.
 GN YEGM OR B2074.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12."
 RL Science 277:1453-1474(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97251358; PubMed=9097040;
 RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y., Sivasubram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horuchi T.;
 RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map."
 RL DNA Res. 3:379-392(1996).
 CC -1- SIMILARITY: BELONGS TO THE ACRA/ACRE FAMILY.
 CC -----
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 CC -----
 DR EMBL: AE000297; AAC75135.1; ALT_INIT.
 DR EMBL: D90845; BAA15928.1; ALT_INIT.
 DR Ecogene: EGI4056; yegm.
 DR InterPro: IPR002215; HLYD.
 DR Pfam: PF00529; HLYD; 1.
 KW Hypothetical protein; Signal; Complete proteome.
 FT SIGNAL 1 21
 FT CHAIN 22 415 HYPOTHETICAL PROTEIN YEGM.
 SQ SEQUENCE 415 AA; 44464 MW; 26240DBBDEDEIA5F CRC64;

Query Match 8.0%; Score 87.5; DB 1; Length 415;
 Best Local Similarity 25.4%; Pred. No. 4;
 Matches 36; Conservative 22; Mismatches 61; Indels 23; Gaps 5;
 OY 58 VSGGSRGKLYAVDFMDKTGT-NNNGPVLRSFYOKVLD-ETGAKKVDIVAHSMGSGANTP 115
 DB 248 VVOAQKAGRPVLEAVDRNKKSLSEGTLLS--LDNQIDATGTGTVKARFNNQDDALFP 305
 OY 116 YVYKN-----LDGKNLENVVTGAGNRSTSKALGTPNOKILYT 157
 DB 306 NOEVNARMVLDPEQNAVITPTALQNGNGCHFWYVNSENKYSKHLVYTGIDQDSQKVVIR 365
 OY 158 STYSSADIMVMYLSKL-DGAK 178
 DB 366 AGISAGDRVAVTDGIDRLTEGAK 387

RESULT 12
 Y045_MYCPN STANDARD: PRT: 485 AA.

AC P75056;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical lipoprotein MG045 homolog precursor (D09_orf485).
 GN MRO058 OR MPO96.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 NC NCBI_TaxID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29342 / M129;
 RX MEDLINE=97105885; PubMed=8948633;
 RA Hammelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 pneumoniae.";
 RL Nucleic Acids Res. 24:4420-4449(1996).
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
 (Potential).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AE000011; AAB95744.1;
 DR InterPro: IPR000044; Lipoprot_8; M045.
 DR Pfam: PF02030; Lipoprotein_8; 1.
 DR PRINTS: PR00905; MYC045.
 DR PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
 KW Hypothetical protein; Lipoprotein; Membrane; Signal;
 KM Complete proteome.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 485 HYPOTHETICAL LIPOPROTEIN MG045 HOMOLOG.
 FT LIPID 23 23 N-ACTYL DIGLYCERIDE (POTENTIAL).
 SQ SEQUENCE 485 AA; 55019 MW; 1AD4E0AB211B64F8 CRC64;
 Query Match 8.0%; Score 87.5; DB 1; Length 485;
 Best Local Similarity 20.9%; Pred. No. 4.9;
 Matches 53; Conservative 34; Mismatches 100; Indels 67; Gaps 9;
 QY 2 KFYRRRIATVITVLSYSLFAMOPSAKAAEHNVVWVHGIGASVYFACIKSYLSOG 61
 DB 27 QFVANESESYSPLLERAE--AKQPMFTLYPTNEKLIINGFANNVTYVAVASVASEL 84
 QY 62 WSRKILAVDWM---DKGTNNNGPVLSRFQKVLDEFGAKKVDVAHSMGANTPY 116
 DB 85 QOQGHLPID-WAKFNLKKTGNSQATIQNKEDAK--ELFTKEIGDISSELLNWGPY 140
 QY 117 YIKNL---DGNKIENVTLLGANSRSTSKALPTDPNOKILYTSYSSADIMVNYLSK 173
 DB 141 FLQDLVEYRGEKIOE-----LEGQDVWSTIIKAIVHKRPNRNLAL 185
 QY 174 LDGAK-----NAQIHGY-----GHIG-----LLMSQ 195
 DB 186 IDDRITFLSLANVHHEVKNFTVDVNPSTGLNFGVYESFANGLKRDMLNTLEVNSD 245
 QY 196 VNSLKEGLNGGQ 209
 DB 246 SNIINELANGRRQ 259
 RESULT 13
 ID BNIL YEAST STANDARD: PRT: 1953 AA.
 AC P41832;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE BNIL protein (Synthetic lethal 39).
 GN BNIL OR SHE5 OR YNL271C OR N0646.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 NC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fares H.F., Pringle J.R.;
 RT "Synthetic lethals of CDC12.";
 RL Submitted (XXX-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-1553 FROM N.A.
 RC STRAIN=S288C / FY1679;
 RX MEDLINE=96310631; PubMed=8740425;
 RT Sen-Gupta M., Lyck R., Fleig U., Niedenthal R.K., Hegemann J.H.;
 RT "The sequence of a 24,152 bp segment from the left arm of chromosome
 RT XIV from Saccharomyces cerevisiae between the BNIL and the POL2
 RT genes.";
 RL Yeast 12:505-514(1996).
 RL [3]
 RP SEQUENCE OF 988-1953 FROM N.A.
 RA Messenguy F., Dubois E., Vierendeels F., Scherens B., Pierard A.,
 RN Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP FUNCTION.
 RX MEDLINE=99187130; PubMed=10085293;
 RA Lee L., Klee S.R., Evangelista M., Boone C., Pellman D.;
 RT "Control of mitotic spindle position by the Saccharomyces cerevisiae
 RT formin Bulp.";
 RL J. Cell Biol. 144:947-961(1999).
 CC -1- FUNCTION: MAY ORGANIZE MICROTUBULES BY MEDIATING SPINDLE
 CC POSITIONING AND MOVEMENT IN THE BUDDING PROCESS. POTENTIAL TARGET
 CC OF THE RHO FAMILY MEMBERS.
 CC -1- SUBUNIT: INTERACTS WITH PROFILIN AT THE FHL DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 GTPASE-BINDING DOMAIN (GBD).
 CC -1- SIMILARITY: CONTAINS 1 FORMIN HOMOLOG 1 (FHL) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 FORMIN HOMOLOG 2 (FH2) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 FORMIN HOMOLOG 3 (FH3) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 DRF AUTOREGULATORY DOMAIN (DAD).
 CC -1- SIMILARITY: BELONGS TO THE FORMIN HOMOLOG FAMILY. BNIL
 CC SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: L31766; AAA34455.1;
 DR EMBL: 271546; CA96178.1;
 DR EMBL: 271547; CA96179.1;
 DR EMBL: X92494; CA63225.1;
 DR SGD: S0005215; BNIL.
 DR InterPro: IPR003104; FH2.
 DR Pfam: PF02181; FH2; 1.
 DR SMART: SM00498; FH2; 1.
 KW Colled coil.
 FT 123 504 GBD.
 FT 356 723 FH3.
 FT 712 807 COILED COIL (POTENTIAL).
 FT 864 894 COILED COIL (POTENTIAL).
 FT 928 981 COILED COIL (POTENTIAL).
 FT 1053 1337 FHL (PRO-RICH).
 FT 1348 1824 FH2.
 FT 1732 1811 COILED COIL (POTENTIAL).
 FT 1799 1813 DAD.
 FT 64 67 POLY-SER.
 FT 1053 1057 POLY-SER.
 FT 1239 1250 POLY-PRO.

FT DOMAIN 1278 1291 POLY-PRO.
 FT DOMAIN 1303 1309 POLY-PRO.
 FT DOMAIN 1751 1754 POLY-GLU.
 FT CONFLICT 938 938 T -> A (IN REF. 1).
 FT CONFLICT 1430 1430 G -> C (IN REF. 1).
 SO SEQUENCE 1953 AA; 219701 MW; A85A994780A5858E CRC64;

Query Match 8.0%; Score 87; DB 1; Length 1953;
 Best Local Similarity 24.3%; Pred. No. 28;
 Matches 49; Conservative 30; Mismatches 79; Indels 50; Gaps 8;

OY 18 SVTSFAMQPSAKAEHNPNVWVGIGASYNFAGIKSYLVSGMSRGLVAVDEMDKTG 77
 DB 233 NTSSTASRTSMASDHPILT-----ANSSLSRKSVMKTSASS-----PTS 275
 OY 78 TNYNNGPVLSPRYOKVLDGTAKKVDIVAHSMGANTPYIKNDGKNIE---NYVTLG 134
 DB 276 TVYSLSLHSTLSSV-----GTSTGKGLVSGLSKQPSLNNITRG 318
 OY 135 GANRSTSKALPCTDPN-----OKILYTSIYSS--ADMIYNNYLSKLDGAKNAQIHGV 185
 DB 319 GAEINTSASTLPGRDTRNRPPIHYVQRILADKLTDSEMKLWLTIRTEQLDWV-DAFIDHQ 377
 OY 186 GHIGL---LMSQVNSLIKEGL 204
 DB 378 GHIAAMVNLMSIYKTPAPRENL 399

RESULT 14

LIP_PSEFR
 ID LIP_PSEFR STANDARD; PRT; 277 AA.
 AC P08658;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).
 OS Pseudomonas fragi.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=296;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-IFO 12049;
 RX MEDLINE=89078617; PubMed=3060375;
 RA Aoyama S., Yoshida N., Inouye S.;
 RT "Cloning, sequencing and expression of the lipase gene from
 Pseudomonas fragi IFO-12049 in E. coli."; FEBS Lett. 242:36-40(1988).
 RL [2]
 RN SEQUENCE OF 1-118 FROM N.A.
 RP STRAIN-IFO 3458;
 RX MEDLINE=87100109; PubMed=3800995;
 RA Kugimiyu W., Otani Y., Hashimoto Y., Takagi Y.;
 RT "Molecular cloning and nucleotide sequence of the lipase gene from
 Pseudomonas fragi."; Biochem. Biophys. Res. Commun. 141:185-190(1986).
 CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
 fatty acid anion.
 CC -1- SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY. PSEUDOMONAS
 LIPASE FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
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 or send an email to license@isb-sib.ch).
 CC EMBL: M14604; AAA25879.1; ALT_SEQ.
 DR EMBL: X14033; CA32193.1; -
 DR PIR: A26383; A26383.

DR PIR: S02005; S02005.
 DR HSSP: 005489; 17AH.
 DR InterPro: IPR000073; Abhydrolase.
 DR InterPro: IPR000734; Lipase.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF00561; abhydrolase_1.
 DR PROSITE: PS00120; Lipase_SER; 1.
 DR Hydrolyase; Lipid degradation; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 277
 FT ACT_SITE 83 83
 FT ACT_SITE 217 217
 FT ACT_SITE 260 260
 SO SEQUENCE 277 AA; 29985 MW; 9A1562BF0772C997 CRC64;

Query Match 8.0%; Score 86.5; DB 1; Length 277;
 Best Local Similarity 26.4%; Pred. No. 3;
 Matches 29; Conservative 21; Mismatches 49; Indels 11; Gaps 4;

OY 36 PYVMVHGIG-----GASYNFAGIKSYLVSGMSRGLVAVDEMDKTGTNYNNGPVLSPRV 90
 DB 10 PILVYHGLGFGRIGSHHFHFGIKQALNECGAS---VFPILISANDNEARGDQLKGI 65
 OY 91 QKVLDETGAKKVDIVAHSMGANTPYIKNDGKNIEENVTLGANGNST 140
 DB 66 HHLRQVGAQRYNLIGHSG-QALTAARYVAAI-APELIASVTSVSGPHGS 113

RESULT 15

MHPC_ECOLI
 ID MHPC_ECOLI STANDARD; PRT; 293 AA.
 AC P77044; P71204; P77205;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 2-hydroxy-6-ketolimon-2,4-dienediolic acid hydrolase (EC 3.7.1.-).
 GN MHPC OR B0349.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / W3110;
 RA Kawamukai M.;
 RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / CS520;
 RA Fernandez A., Garcia J.L., Diaz E.;
 RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
 RL [4]
 RN SEQUENCE FROM N.A.
 RP STRAIN-K12 / MG1655;
 RA Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K.,
 RA Federspiel N., Hyman R., Kaiman S., Komp C., Kirdi O., Lew H., Lin D.,
 RA Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
 RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- PATHWAY: 3-hydroxyphenylpropanate degradation.
 CC -1- SIMILARITY: STRONG, TO B.CEPACIA AND PSEUDOMONAS BPHD.
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Db      60  WGSNKLALDYFDKGTGNNLNNGPQLASVDVLTETGAKKVDIVAHSMGANTLYIKTL 119
      122  DGGNKIENVVTLGGANRSTTSKALPCTDPNOKILYTSISSADMIYMTLSKIDGAKNAQ 181
      120  GGGNKIQNVVTLGGANGVLSTALPCTDPNOKILYTSIYSLNDQIYINLSRLOGARNTQ 179
      182  HGVGHIGILMNSQVNSLIKEGNGGQNTN 212
      180  LYGIGHIGILMNSQVNGYIKKGLNGGLMTN 210

RESULT 4
Q9RJP5  PRELIMINARY:      PRT:      210 AA.
ID      08RJP5  PRELIMINARY:      PRT:      210 AA.
AC      08RJP5  PRELIMINARY:      PRT:      210 AA.
DT      01-JUN-2002 (TREMBlrel. 21, Created)
DT      01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT      01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE      Extracellular esterase precursor (EC 3.1.1.1).
GN      LIPA.
OS      Bacillus megaterium.
OC      Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC      Bacillaceae; Bacillus.
OX      NCBI_TaxID=1404;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=ATCC9885;
RA      Ruiz C., Pastor J., Diaz P.;
RT      "Identification and cloning of Bacillus megaterium and Bacillus sp.
RT      BP-6 esterases. Comparison with Bacillus subtilis and Bacillus pumilus
RT      lipases."
RL      Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
DR      EMBL: AJ430831; CAD23620.1;
KM      Signal; Hydrolase.
FT      SIGNAL 1 28
FT      CHAIN 1 210
FT      SEQUENCE 210 AA; 22411 MW; 94089898826918 CRC64;

Query Match      66.1%; Score 719.5; DB 2; Length 210;
Best Local Similarity 67.3%; Pred. No. 5.5e-49;
Matches 142; Conservative 24; Mismatches 42; Indels 3; Gaps 2;

QY      4  VKRRITATVTLVSLTSLFAMQPSAKAAE--HNPVVMVHGIGGASYNFAGIKSYLVSOQ 61
      1  MKKVLAFILICSL-ILSYLAAPPSCAKAESVHNPPVLVHGIGGASYNFALIKNYLISOG 59
      62  WSRGKIYAVDFDKGTGNNLNNGPQLASVDVLTETGAKKVDIVAHSMGANTLYIKTL 121
      60  WGSNKLALDYFDKGTGNNLNNGPQLASVDVLTETGAKKVDIVAHSMGANTLYIKTL 119
      122  DGGNKIENVVTLGGANRSTTSKALPCTDPNOKILYTSISSADMIYMTLSKIDGAKNAQ 181
      120  GGGNKIQNVVTLGGANGVLSTALPCTDPNOKILYTSIYSLNDQIYINLSRLOGARNTQ 179
      182  HGVGHIGILMNSQVNSLIKEGNGGQNTN 212
      180  LYGIGHIGILMNSQVNGYIKKGLNGGLMTN 210

RESULT 5
Q9RSP6  PRELIMINARY:      PRT:      237 AA.
ID      09RSP6  PRELIMINARY:      PRT:      237 AA.
AC      09RSP6  PRELIMINARY:      PRT:      237 AA.
DT      01-MAY-2000 (TREMBlrel. 13, Created)
DT      01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT      01-MAY-2000 (TREMBlrel. 20, Last annotation update)
DE      Lipase, putative.
GN      DR2078.
OS      Deinococcus radiodurans.
OC      Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC      Deinococcaceae; Deinococcus.
OX      NCBI_TaxID=1259;

```

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RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=R1;
RX      MEDLINE=20036896; PubMed-10567266;
RA      White O., Eissen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA      Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA      Moffat K.S., Qin H., Jiang L., Pamphile M., Crosby M., Shen M.,
RA      Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA      Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA      Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA      Fraser C.M.;
RT      "Genome sequence of the radioresistant bacterium Deinococcus
RT      radiodurans R1."
RL      Science 286:1571-1577 (1999).
DR      EMBL: AE002044; AAF11628.1;
DR      TIGR: DR2078;
DR      InterPro: IPR002918; Lipase-2.
DR      InterPro: IPR000379; Ser_estrs_site.
DR      Pfam: PF01674; Lipase_2; 1.
KM      Complete proteome.
SQ      SEQUENCE 237 AA; 25308 MW; 1C2BF99210B8AF2E CRC64;

Query Match      19.1%; Score 208; DB 16; Length 237;
Best Local Similarity 26.6%; Pred. No. 1.1e-08;
Matches 61; Conservative 47; Mismatches 93; Indels 28; Gaps 6;

QY      1  MKFVKRRITATVTLVSLTSLFAMQPSAKAAE-----HNPVVMVHGIGGASYNFAGIK 54
      6  LAFSKRFVLLPISALACCGTITQAPSELDAQALAAPVRHPLFVHGNSDGSITSPMM 65
      55  SYLVSOQWSRGKIYAVDFDKGTGNNLNNGPQLASVDVLTETGAKKVDIVAHSMGANT 114
      66  NRRKQGWTDQALFMSY--DSFKSNVATDLRQKDALIAQGAQVQIVSHMGALSS 124
      115  PYIKKLDDGKNKIENVVTLGGANR-----STTS-----KAL-PCTDPNOKI 154
      125  RYLLKMLGGTAKDAVWSLGGPNHGTDFALCASCIEMRGSSPRTKALNSGDETPGAV 184
      155  LYSIYSSADMIY-MNYLSKIDGAKNAQIHGVGHIGILMNSQVNSLIKE 202
      185  RYATWMSPCDVAIVNPSSVPLSGATNTKTSCLTHSSLYGDATVYTYOVRD 233

RESULT 6
Q9KY65  PRELIMINARY:      PRT:      331 AA.
ID      09KY65  PRELIMINARY:      PRT:      331 AA.
AC      09KY65  PRELIMINARY:      PRT:      331 AA.
DT      01-OCT-2000 (TREMBlrel. 15, Created)
DT      01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT      01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE      Putative secreted lipase.
GN      SC04799 OR SC063A.10C.
OS      Streptomyces coelicolor.
OC      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC      Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
OX      NCBI_TaxID=1902;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=A3(2);
RA      Brown S.P., Harris D.;
RL      Submitted (May-2000) to the EMBL/Genbank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=A3(2);
RA      Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL      Submitted (May-2000) to the EMBL/Genbank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=A3(2);
RX      MEDLINE=97000351; PubMed=8643436;
RA      Redenbach M., Kiese R.H.M., Denapalpe D., Eichner A., Cullum J.,
RA      Kinsahl H., Hopwood D.A.;
RT      "A set of ordered cosmids and a detailed genetic and physical map for

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RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2) / M145;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 Huang C.-H., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 Rabinowitsch E., Rajandream M.A., Rutherford K., Ruter S.,
 Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
 Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL: AL356832; CAB92662.1; -
 DR InterPro: IPR000734; Lipase.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR PROSITE: PS00120; LIPASE_SER; 1.
 DR PROSITE: PS00120; LIPASE_SER; 1.
 SO SEQUENCE 331 AA; 35137 MW; 3E0E77A68747211 CRC64;
 Query Match 16.7%; Score 181.5; DB 16; Length 331;
 Best Local Similarity 25.6%; Pred. No. 2.1e-06;
 Matches 54; Conservative 42; Mismatches 86; Indels 29; Gaps 6;
 Oy 27 PSAAAEHNPVVMVIGIGASYNFAGIKSYLSQSGMRGKLYAVDFWDRKGTNNNGPVL 86
 Db 106 PRPARAPRVLVHGFIDNSVFLRLSLAONG-RHAIESLVNSPLTCDIRTAELL 163
 Oy 87 SRPVOKVLEDTGAKKVDIVAHSMGANTPYIKNIDGKNKIENVTLGANGSTSKAL- 145
 Db 164 GRHIEIEICERGSEKVDVGHSLGLIARYVORLGGDLRVFTLVLTCTPHGTGVVPLA 223
 Oy 146 -----GFT-----DPNQKILYTSVSSADMIYNNYLSK--LD---GAKNA 180
 Db -224 NAHPIVRQMRPESAVIEELTRAPACCRTRFVSFWSDLR-VMDPLETACLDHPLDSQV 282
 Oy 181 QIHGVGHIGLIMNSQVNSLIRKELGGGGONT 211
 Db 283 RVSGIGHLALPVHAPVATGIRQALDTACRPET 313
 RESULT 7
 Q9S295 PRELIMINARY; PRT; 290 AA.
 ID Q9S295;
 AC Q9S295;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative secreted lipase.
 GN SC01735 OR SC011.24C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Saunders D., Harris D.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA MEDLINE=97000351; Pubmed=8843436;
 RX Redenbach M., Kieser H.M., Denapalte D., Eichner A., Cullum J.,
 Kinashi H., Hopwood D.A.;

RT "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2) / M145;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 Huang C.-H., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 Rabinowitsch E., Rajandream M.A., Rutherford K., Ruter S.,
 Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
 Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL: AL096849; CAB50950.1; -
 DR HSSP; Q05489; 17AH.
 DR InterPro: IPR002918; Lipase_2.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF01674; Lipase_2; 1.
 SO SEQUENCE 290 AA; 30496 MW; D56E8508350F7432 CRC64;
 Query Match 16.4%; Score 178; DB 16; Length 290;
 Best Local Similarity 28.6%; Pred. No. 3.3e-06;
 Matches 57; Conservative 30; Mismatches 62; Indels 50; Gaps 8;
 Oy 23 FAMQSAKAENHPVVMVIGIGASYNFAGIKSYLSQSGMRGKLYAVDFWDRKGTNN- 79
 Db 45 YTKAPS--AAHPRVVLVHGFIDNSVFLRLSLAONG--VFSLDGLGOLPGVLF 99
 Oy 80 YNNGPV-----LSRFVOKVLEDTGAKKVDIVAHSMGANTPYIKNIDGKNKIENVTL 133
 Db 100 HGLSPVEKSAEGLAHNVKVLAAATGATETDLVGHSGGMPPRYIKFLGAAEVVALGI 159
 Oy 134 GGANSTT-----SKALP-----GTPNQKILYTS 158
 Db 160 APSNNGTTLGSLTRLLPFGAEDLNEHTPALADQVGVSVLRLNAGGTPGVRTV 219
 Oy 159 IYSSADMIYNNYLSK-LDG 176
 Db 220 LATKYDEVVTPRGQFLDG 238
 RESULT 8
 Q8RC83 PRELIMINARY; PRT; 403 AA.
 ID Q8RC83;
 AC Q8RC83;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Predicted acetyltransferases and hydrolases with the alpha/beta
 hydrolase fold.
 GN LIPA OR TRE0555.
 OS Thermomacrobacter tengcongensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Thermomacrobacteriales; Thermomacrobacteriaceae; Thermomacrobacter.
 OX NCBI_TaxID=119072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MB4T / JCM11007;
 RX MEDLINE=21992816; Pubmed=11997336;
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
 Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
 Tan H., Chen R., Wang J., Yu J., Yang H.;
 RT "A complete sequence of T. tengcongensis genome.";
 RL Genome Res. 12:689-700(2002).
 DR EMBL: AE013025; AAM23831.1; -
 KW Transferase; Hydrolase; Complete proteome.
 SO SEQUENCE 403 AA; 45221 MW; DC31D5E86EC2CAC4 CRC64;

Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.


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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Brown S.P., Harris D.;
RL Submitted (Jul-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (Jul-2000) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA MEDLINE-97000351; PubMed-8843436;
RA Redenbach M., Kieser H.M., Denapalte D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinovich E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL: AL390188; CAB99145.1;
DR InterPro: IPR002918; Lipase_2.
DR InterPro: IPR000379; Ser-estrs_site.
DR Pfam: PF01674; Lipase_2; 1.
SQ SEQUENCE 289 AA; 31466 MW; 03D9002A2040FD52 CRC64;

Query Match 13.4%; Score 145.5; DB 16; Length 289;
Best Local Similarity 23.8%; Pred. No. 0.0012;
Matches 55; Conservative 35; Mismatches 76; Indels 65; Gaps 10;

QY 33 EH-NPVMVHG-IGGASYNFAGIKSYLVSGMSRGLYAVDFWDK-----TGTNNNG 83
DB 58 EHRPRVVLVHGTGFGNGYTMNTAVPLLRHG--HVFRLDYGQGNPLIFGLGDIKHA 114
QY 84 PVLSEFVQKVLDETGAKKVDIYAHSMGANTPYIYKNDGKNIENVVTLGANNSTSK 143
DB 115 RQLAEFVEVLRTGTGAQVDLVFGSGGMPRYLYNALGGPKVHNFVGISPSNGHTAQ 174
QY 144 AL-----PGT-----DPNOKILYTSIYSSA 163
DB 175 GLMNLARQIFGAVELLECGAVGEVVPWPQLQHDHLFORELADLGTTGCVRRHTVATQY 234
QY 164 DMIYVNY-----LSKLDG--AKNAQIHGV-----HIGLMSQV-NSLIK 201
DB 235 DDVVPYPTSCALAKTEGCVNNIVLQDIDPDHPTVSMYNAVYLVNLEVK 285

RESULT 15
ID Q8YX63 PRELIMINARY; PRT; 211 AA.
AC Q8YX63;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical protein ALR1352.
GN ALR1352.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21595285; PubMed-11759840;
RA Kaneko T., Nakamura Y., Molk C.P., Kurita T., Sasamoto S.,
RA Watanabe A., Iriuchij M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL: AP003585; BAB73309.1;
DR InterPro: IPR002047; AKH.
DR InterPro: IPR002918; Lipase_2.
DR InterPro: IPR000379; Ser-estrs_site.
DR Pfam: PF01674; Lipase_2; 1.
DR PROSITE: PS00256; AKH; UNKNOWN.1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 211 AA; 23718 MW; 08A8720935DA8F75 CRC64;

Query Match 13.3%; Score 145; DB 16; Length 211;
Best Local Similarity 26.5%; Pred. No. 0.00084;
Matches 54; Conservative 33; Mismatches 77; Indels 40; Gaps 8;

QY 33 EHNPMVVMHIGGASYNFAGIKSYLVSGMSRGLYAVDFWDKTGTNNNGPY-LSRFVQ 91
DB 7 GRNPVLLVGHITDTEVFNPMAVYLRLQGLMTYTLNLV-----NNGEAPLVNLAQ 57
QY 92 KYLDE-----TGAKKVDIYAHSMGANTPYIYKNDGKNIENVVTLGANNST--SK 143
DB 58 QADVVCATITPEQPELDLVFGSMGIVSRYYQKLGISRYORFVYISSPHHGTVVAVAS 117
QY 144 ALPG---TDPN-----OKILYTSIYSSAD-MIYVNYLSKLDGAKNAQIHGV 185
DB 118 QHRCQGMQRPNSLFLQDLNRDVQMLEQLNFTSIWTFYDLMIITPHSSKAPVGRKELTIPVA 177
QY 186 GHIGLIMN-----SQVNSLIKEGLN 205
DB 178 LHSWMLKDFRSIEVAVNALAEPIIN 201

Search completed: May 9, 2003, 16:21:56
Job time : 34 secs

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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2003, 04:58:28 ; Search time 1429 seconds

(without alignments)
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Title: US-09-905-666a-1

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Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb-ba:*
2: gb-hcg:*
3: gb-in:*
4: gb-om:*
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10: gb-ro:*
11: gb-sts:*
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14: gb-vi:*
15: em-ba:*
16: em-fun:*
17: em-hum:*
18: em-in:*
19: em-mu:*
20: em-om:*
21: em-or:*
22: em-ov:*
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24: em-ph:*
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40: em-htgo-mus:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	639	100.0	639	6	AX418871 Sequence
2	629.4	98.5	639	6	AX418877 Sequence
3	627.8	98.2	639	6	AX418878 Sequence
4	626.2	98.0	639	6	AX365571 Sequence
5	626.2	98.0	639	6	AX418874 Sequence
6	626.2	98.0	639	6	AX418875 Sequence
7	623	97.5	639	6	AX418876 Sequence
8	606.4	94.9	639	6	AX418873 Sequence
9	573.4	89.7	35000	1	AB000617 Bacillus
10	573.4	89.7	221160	1	BSUB0002
11	571.8	89.5	1495	1	BACLPASE
12	565.4	88.5	639	6	A02813
13	565.4	88.5	1831	6	A02815
14	565.4	88.5	1831	6	A02816
15	564.4	88.3	639	6	AX418872 Sequence
16	562.2	88.0	639	6	AX418879 Sequence
17	523.2	81.9	544	6	AX418894 Sequence
18	523.2	81.9	544	6	AX418923 Sequence
19	523.2	81.9	544	6	AX418924 Sequence
20	521.6	81.6	544	6	AX418913 Sequence
21	521.6	81.6	544	6	AX418916 Sequence
22	518.4	81.1	544	6	AX418896 Sequence
23	518.4	80.9	544	6	AX418915 Sequence
24	516.8	80.9	544	6	AX418910 Sequence
25	515.2	80.6	544	6	AX418904 Sequence
26	515.2	80.6	544	6	AX418914 Sequence
27	515.2	80.6	544	6	AX418922 Sequence
28	514.2	80.5	639	6	AX418886 Sequence
29	512.6	80.2	639	6	AX418885 Sequence
30	512	80.1	544	6	AX418903 Sequence
31	510.4	79.9	544	6	AX418893 Sequence
32	510.4	79.9	544	6	AX418900 Sequence
33	509.4	79.7	639	6	AX418884 Sequence
34	508.8	79.6	544	6	AX418912 Sequence
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36	507.2	79.4	544	6	AX418891 Sequence
37	505.6	79.1	544	6	AX418892 Sequence
38	505.6	79.1	544	6	AX418898 Sequence
39	505.6	79.1	544	6	AX418901 Sequence
40	504	78.9	544	6	AX418897 Sequence
41	504	78.9	544	6	AX418920 Sequence
42	500.8	78.4	544	6	AX418921 Sequence
43	499.2	78.1	544	6	AX418899 Sequence
44	499.2	78.1	544	6	AX418918 Sequence
45	496	77.6	544	6	AX418902 Sequence

ALIGNMENTS

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LOCUS AX418871 639 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 1 from Patent WO0206457.
ACCESSION AX418871
VERSION AX418871.1 GI:21523726
KEYWORDS
SOURCE
ORGANISM Bacillus pumilus.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

REFERENCE 1
AUTHORS Giver, L.J., Minshull, J. and Vogel, K.
TITLE Novel lipase genes
JOURNAL Patent: WO 0206457-A 1 24-JAN-2002;
Maxygen, Inc. (US)

FEATURES
Source Location/Qualifiers
1. 639
/organism="Bacillus pumilus"
/db_xref="taxon:1408"

BASE COUNT 201 a 123 c 159 g 156 t

ORIGIN

Query Match 100.0%; Score 639; DB 6; Length 639;
Best Local Similarity 100.0%; Pred. No. 1.4e-184;
Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGAAATTTGTAAGAGATCATTCAGTCTTGTACAAATTTGGTCTCTAGTACA 60
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OY 61 TCGGTGTTGGATGACAGCCGTCAGCAAAAGCCGTCGAACAAATCCAGTTGTTAGTT 120
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DB 61 TCGGTGTTGGATGACAGCCGTCAGCAAAAGCCGTCGAACAAATCCAGTTGTTAGTT 120
|||||
OY 121 CACGGTATCGAGAGACTTCTACAAATTTTGGGGAATTAAGACCTATCTGTATCTCAG 180
|||||
DB 121 CACGGTATCGAGAGACTTCTACAAATTTTGGGGAATTAAGACCTATCTGTATCTCAG 180
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OY 181 GCGTGTACAGGGGCAAGCTGTATGCGGTGATTTTGGGCAAGACAGGAGCAATTTAT 240
|||||
DB 181 GCGTGTACAGGGGCAAGCTGTATGCGGTGATTTTGGGCAAGACAGGAGCAATTTAT 240
|||||
OY 241 AACATGCCCCGATATATACAGATTTGTGCAAAAGTTTGAAGCAAAAGCGTGCAGAA 300
|||||
DB 241 AACATGCCCCGATATATACAGATTTGTGCAAAAGTTTGAAGCAAAAGCGTGCAGAA 300
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OY 301 AAATGATATTTGCTGCACAGATGAGTGGGCGGCAACACACTTACTACATATAAAAT 360
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DB 301 AAATGATATTTGCTGCACAGATGAGTGGGCGGCAACACACTTACTACATATAAAAT 360
|||||
OY 361 CTGACGCGCGGAATTAATTAAGAAAGCTGTAAAGCTTGGCGGCGCAACGTTGACG 420
|||||
DB 361 CTGACGCGCGGAATTAATTAAGAAAGCTGTAAAGCTTGGCGGCGCAACGTTGACG 420
|||||
OY 421 ACAAGCAAGGCGCTTCCGGGAACAGATCCAATCAAAAGATTTTATACATCCATTTAC 480
|||||
DB 421 ACAAGCAAGGCGCTTCCGGGAACAGATCCAATCAAAAGATTTTATACATCCATTTAC 480
|||||
OY 481 AGCAGTCCGATATGATGTCATGATTAATTAAGAGCGGTCTAAAAAGCCT 540
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DB 481 AGCAGTCCGATATGATGTCATGATTAATTAAGAGCGGTCTAAAAAGCCT 540
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OY 541 CAATTCATGCGCTTGGGCAATTTGTTTATGATGAACAGCCAAAGTCAACAGCCTGATT 600
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DB 541 CAATTCATGCGCTTGGGCAATTTGTTTATGATGAACAGCCAAAGTCAACAGCCTGATT 600
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OY 601 AAAGAGACTGAACGCGGGGCGCAAAATACGAATTAA 639
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DB 601 AAAGAGACTGAACGCGGGGCGCAAAATACGAATTAA 639
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RESULT 2
AX41877 639 bp DNA linear PAT 18-JUN-2002
LOCUS AX41877
DEFINITION Sequence 7 from Patent WO0206457.
ACCESSION AX41877
VERSION AX41877.1 GI:21523732
KEYWORDS
SOURCE Bacillus firmus.
ORGANISM Bacillus firmus.
REFERENCE 1
AUTHORS Giver, L.J., Minshull, J. and Vogel, K.
TITLE Novel lipase genes
JOURNAL Patent: WO 0206457-A 7 24-JAN-2002;
Maxygen, Inc. (US)
FEATURES
source Location/Qualifiers
1. 639

FEATURES
Source Location/Qualifiers
1. 639
/organism="Bacillus firmus"
/db_xref="taxon:1399"

BASE COUNT 202 a 123 c 157 g 157 t

ORIGIN

Query Match 98.5%; Score 629.4; DB 6; Length 639;
Best Local Similarity 99.1%; Pred. No. 1.2e-181;
Matches 633; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 ATGAAATTTGTAAGAGATCATTCAGTCTTGTACAAATTTGGTCTCTAGTACA 60
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DB 1 ATGAAATTTGTAAGAGATCATTCAGTCTTGTACAAATTTGGTCTCTAGTACA 60
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OY 61 TCGGTGTTGGATGACAGCCGTCAGCAAAAGCCGTCGAACAAATCCAGTTGTTAGTT 120
|||||
DB 61 TCGGTGTTGGATGACAGCCGTCAGCAAAAGCCGTCGAACAAATCCAGTTGTTAGTT 120
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OY 121 CACGGTATCGAGAGACTTCTACAAATTTTGGGGAATTAAGACCTATCTGTATCTCAG 180
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DB 121 CACGGTATCGAGAGACTTCTACAAATTTTGGGGAATTAAGACCTATCTGTATCTCAG 180
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OY 181 GCGTGTACAGGGGCAAGCTGTATGCGGTGATTTTGGGCAAGACAGGAGCAATTTAT 240
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DB 181 GCGTGTACAGGGGCAAGCTGTATGCGGTGATTTTGGGCAAGACAGGAGCAATTTAT 240
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OY 241 AACATGCCCCGATATATACAGATTTGTGCAAAAGTTTGAAGCAAAAGCGTGCAGAA 300
|||||
DB 241 AACATGCCCCGATATATACAGATTTGTGCAAAAGTTTGAAGCAAAAGCGTGCAGAA 300
|||||
OY 301 AAATGATATTTGCTGCACAGATGAGTGGGCGGCAACACACTTACTACATATAAAAT 360
|||||
DB 301 AAATGATATTTGCTGCACAGATGAGTGGGCGGCAACACACTTACTACATATAAAAT 360
|||||
OY 361 CTGACGCGCGGAATTAATTAAGAAAGCTGTAAAGCTTGGCGGCGCAACGTTGACG 420
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DB 361 CTGACGCGCGGAATTAATTAAGAAAGCTGTAAAGCTTGGCGGCGCAACGTTGACG 420
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OY 421 ACAAGCAAGGCGCTTCCGGGAACAGATCCAATCAAAAGATTTTATACATCCATTTAC 480
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DB 421 ACAAGCAAGGCGCTTCCGGGAACAGATCCAATCAAAAGATTTTATACATCCATTTAC 480
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OY 481 AGCAGTCCGATATGATGTCATGATTAATTAAGAGCGGTCTAAAAAGCCT 540
|||||
DB 481 AGCAGTCCGATATGATGTCATGATTAATTAAGAGCGGTCTAAAAAGCCT 540
|||||
OY 541 CAATTCATGCGCTTGGGCAATTTGTTTATGATGAACAGCCAAAGTCAACAGCCTGATT 600
|||||
DB 541 CAATTCATGCGCTTGGGCAATTTGTTTATGATGAACAGCCAAAGTCAACAGCCTGATT 600
|||||
OY 601 AAAGAGACTGAACGCGGGGCGCAAAATACGAATTAA 639
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DB 601 AAAGAGACTGAACGCGGGGCGCAAAATACGAATTAA 639
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RESULT 3
AX41878 639 bp DNA linear PAT 18-JUN-2002
LOCUS AX41878
DEFINITION Sequence 8 from Patent WO0206457.
ACCESSION AX41878
VERSION AX41878.1 GI:21523733
KEYWORDS
SOURCE Bacillus badius.
ORGANISM Bacillus badius.
REFERENCE 1
AUTHORS Giver, L.J., Minshull, J. and Vogel, K.
TITLE Novel lipase genes
JOURNAL Patent: WO 0206457-A 8 24-JAN-2002;
Maxygen, Inc. (US)
FEATURES
source Location/Qualifiers
1. 639
/organism="Bacillus badius"
/db_xref="taxon:1455"

BASE COUNT 202 a 122 c 157 g 158 t
ORIGIN

Query Match 98.2%; Score 627.8; DB 6; Length 639;
Best Local Similarity 98.9%; Pred. No. 3.8e-181;
Matches 632; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 ATGAATTTGTAAAAAGAGATCATTTGCACTTGTAAACATTTTGGTGTCTGACACACA 60
DB 1 ATGAATTTGTAAAAAGAGATCATTTGCACTTGTAAACATTTTGGTGTCTGACACACA 60
OY 61 TCGCTTTTGGCATGACGCGTCAGCAAAAGCCGTTGAACACATCCAGTTGTTAGTT 120
DB 61 TCGCTTTTGGCATGACGCGTCAGCAAAAGCCGTTGAACACATCCAGTTGTTAGTT 120
OY 121 CACGGTATCGAGAGACCTTCATCAATTTTGGGGGAATTAAGCGTATCTCGTATCTCAG 180
DB 121 CACGGTATCGAGAGACCTTCATCAATTTTGGGGGAATTAAGCGTATCTCGTATCTCAG 180
OY 181 GCGTGTACAGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAAGACAGGAGCAATTA 240
DB 181 GCGTGTACAGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAAGACAGGAGCAATTA 240
OY 241 AACATGCGCCGCTATTCACAGATTGTGCAAAAGCTTTTGAACGAAAGGGGTGCGAAA 300
DB 241 AACATGCGCCGCTATTCACAGATTGTGCAAAAGCTTTTGAACGAAAGGGGTGCGAAA 300
OY 301 AAAGTGTATTTGCTGCTACAGTATGGGCGGCAACACACCTTACTATCAATAAAAAT 360
DB 301 AAAGTGTATTTGCTGCTACAGTATGGGCGGCAACACACCTTACTATCAATAAAAAT 360
OY 361 CTGGACGGCGGAATTAATTAAGAAAGCTGTAACGCTTGGCGGCGCAACCGTTGCAAG 420
DB 361 CTGGACGGCGGAATTAATTAAGAAAGCTGTAACGCTTGGCGGCGCAACCGTTGCAAG 420
OY 421 ACAAGCAAGCGCTTCCGGGAACAGATCCAATCAAAAGATTTTATACATTCATTTAC 480
DB 421 ACAAGCAAGCGCTTCCGGGAACAGATCCAATCAAAAGATTTTATACATTCATTTAC 480
OY 481 ASCAGTCCGATATGATGCTATGATTAATTAATTAAGCGTCTTAAAAAGCGT 540
DB 481 ASCAGTCCGATATGATGCTATGATTAATTAATTAAGCGTCTTAAAAAGCGT 540
OY 541 CAAATTCATGCGGTTGGGACATTTGTTATGATGAACAGCCAGCTGATTT 600
DB 541 CAAATTCATGCGGTTGGGACATTTGTTATGATGAACAGCCAGCTGATTT 600
OY 601 AAAGAAGGACTGACGCGCGGAGCCCAATACAAATTA 639
DB 601 AAAGAAGGACTGACGCGCGGAGCCCAATACAAATTA 639

RESULT 4

AX365571 639 bp DNA linear PAT 15-FEB-2002

LOCUS AX365571 Sequence 2 from Patent WO0200232.

DEFINITION AX365571

ACCESSION AX365571

VERSION AX365571.1 GI:18697126

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

/note="lipase 396"
/codon_start=1
/transl_table=1
/protein_id="CAD23819.1"
/db_xref="GI:18697127"

Query Match 98.0%; Score 626.2; DB 6; Length 639;
Best Local Similarity 98.7%; Pred. No. 1.2e-180;
Matches 631; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 ATGAATTTGTAAAAAGAGATCATTTGCACTTGTAAACATTTTGGTGTCTGACACACA 60
DB 1 ATGAATTTGTAAAAAGAGATCATTTGCACTTGTAAACATTTTGGTGTCTGACACACA 60
OY 61 TCGCTTTTGGCATGACGCGTCAGCAAAAGCCGTTGAACACATCCAGTTGTTAGTT 120
DB 61 TCGCTTTTGGCATGACGCGTCAGCAAAAGCCGTTGAACACATCCAGTTGTTAGTT 120
OY 121 CACGGTATCGAGAGACCTTCATCAATTTTGGGGGAATTAAGCGTATCTCGTATCTCAG 180
DB 121 CACGGTATCGAGAGACCTTCATCAATTTTGGGGGAATTAAGCGTATCTCGTATCTCAG 180
OY 181 GCGTGTACAGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAAGACAGGAGCAATTA 240
DB 181 GCGTGTACAGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAAGACAGGAGCAATTA 240
OY 241 AACATGCGCCGCTATTCACAGATTGTGCAAAAGCTTTTGAACGAAAGGGGTGCGAAA 300
DB 241 AACATGCGCCGCTATTCACAGATTGTGCAAAAGCTTTTGAACGAAAGGGGTGCGAAA 300
OY 301 AAAGTGTATTTGCTGCTACAGTATGGTGGCGGCAACACACCTTACTATCAATAAAAAT 360
DB 301 AAAGTGTATTTGCTGCTACAGTATGGTGGCGGCAACACACCTTACTATCAATAAAAAT 360
OY 361 CTGGACGGCGGAATTAATTAAGAAAGCTGTAACGCTTGGCGGCGCAACCGTTGCAAG 420
DB 361 CTGGACGGCGGAATTAATTAAGAAAGCTGTAACGCTTGGCGGCGCAACCGTTGCAAG 420
OY 421 ACAAGCAAGCGCTTCCGGGAACAGATCCAATCAAAAGATTTTATACATTCATTTAC 480
DB 421 ACAAGCAAGCGCTTCCGGGAACAGATCCAATCAAAAGATTTTATACATTCATTTAC 480
OY 481 ASCAGTCCGATATGATGCTATGATTAATTAATTAAGCGTCTTAAAAAGCGT 540
DB 481 ASCAGTCCGATATGATGCTATGATTAATTAATTAAGCGTCTTAAAAAGCGT 540
OY 541 CAAATTCATGCGGTTGGGACATTTGTTATGATGAACAGCCAGCTGATTT 600
DB 541 CAAATTCATGCGGTTGGGACATTTGTTATGATGAACAGCCAGCTGATTT 600
OY 601 AAAGAAGGACTGACGCGCGGAGCCCAATACAAATTA 639
DB 601 AAAGAAGGACTGACGCGCGGAGCCCAATACAAATTA 639

RESULT 5

AX418874 639 bp DNA linear PAT 18-JUN-2002

LOCUS AX418874 Sequence 4 from Patent WO0206457.

DEFINITION AX418874

ACCESSION AX418874

VERSION AX418874.1 GI:21523729

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

TITLE Novel Lipase genes
JOURNAL Patent: WO 0206457-A 4 24-JAN-2002;
Maxygen, Inc. (US)
FEATURES Location/Qualifiers
source 1..639
/organism="Bacillus lentus"
/db_xref="taxon:1467"

BASE COUNT 203 a 120 c 157 g 159 t
ORIGIN

Query Match 98.0%; Score 626.2; DB 6; Length 639;
Best Local Similarity 98.7%; Pred. No. 1.2e-180;
Matches 631: Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ATGAATTTGTAAGAGAGATCATTCCTGTATACAAATTTGGTCTGCTACATCA 60
Db 1 ATGAATTTGTAAGAGAGATCATTCCTGTATACAAATTTGGTCTGCTACATCA 60
QY 61 TCGCTGTTGGATGACACCGCTCAGCAAAAGCCGCTGAACCAATCCAGTTGTATG 120
Db 61 TCGCTGTTGGATGACACCGCTCAGCAAAAGCCGCTGAACCAATCCAGTTGTATG 120
QY 121 CACGATATCGAGAGAGCTTCATACAAATTTGGGGAATTAAGAGCTATCTGATCTCAG 180
Db 121 CACGATATCGAGAGAGCTTCATACAAATTTGGGGAATTAAGAGCTATCTGATCTCAG 180
QY 181 GCGTGTACGCGGCGACGCTGTATGCGGTTGATTTGGGACAGACAGGAGCAATTTAT 240
Db 181 GCGTGTACGCGGCGACGCTGTATGCGGTTGATTTGGGACAGACAGGAGCAATTTAT 240
QY 241 AACATGCCCCGGTATTTATCAGATTTGTGCAAAAGTTTAAAGCAAGCGGTCGAAA 300
Db 241 AACATGCCCCGGTATTTATCAGATTTGTGCAAAAGTTTAAAGCAAGCGGTCGAAA 300
QY 301 AAAGTGATTTGTCGCTACAGATTTGGTGGCGGAGACACCTTACTACATAAAAT 360
Db 301 AAAGTGATTTGTCGCTACAGATTTGGTGGCGGAGACACCTTACTACATAAAAT 360
QY 361 CTGACGCGGGAATTAATTTGAAGAGCTGTACGCTTTGGCGGCGAACCCTTGACG 420
Db 361 CTGACGCGGGAATTAATTTGAAGAGCTGTACGCTTTGGCGGCGAACCCTTGACG 420
QY 421 ACAAGCAAGGCGCTCCGGAACAGATCCAAATCAAAAGATTTTATACATCCATTAC 480
Db 421 ACAAGCAAGGCGCTCCGGAACAGATCCAAATCAAAAGATTTTATACATCCATTAC 480
QY 481 AGCAGTCCGATATGATTTGTCATGAATTAATTAAGAGCGGTCTAAACGCT 540
Db 481 AGCAGTCCGATATGATTTGTCATGAATTAATTAAGAGCGGTCTAAACGCT 540
QY 541 CAAATTCATGGCGTTGGGACATTTGTTATGATGAACAGCCAAAGCTGATTT 600
Db 541 CAAATTCATGGCGTTGGGACATTTGTTATGATGAACAGCCAAAGCTGATTT 600
QY 601 AAAGAAGAGCTGAACGCGGCGGCAAAATACGAATTA 639
Db 601 AAAGAAGAGCTGAACGCGGCGGCAAAATACGAATTA 639

RESULT 6
AX418875 639 bp DNA Linear PAT 18-JUN-2002
LOCUS AX418875
DEFINITION Sequence 5 from Patent WO0206457.
ACCESSION AX418875
VERSION AX418875.1 GI:21523730
KEYWORDS
SOURCE Bacillus circulans.
ORGANISM Bacillus circulans
REFERENCE 1
AUTHORS Giver, L.J., Minshull, J. and Vogel, K.
TITLE Novel Lipase genes
JOURNAL Patent: WO 0206457-A 5 24-JAN-2002;

Maxygen, Inc. (US)
FEATURES Location/Qualifiers
source 1..639
/organism="Bacillus circulans"
/db_xref="taxon:1397"

BASE COUNT 201 a 122 c 157 g 159 t
ORIGIN

Query Match 98.0%; Score 626.2; DB 6; Length 639;
Best Local Similarity 98.7%; Pred. No. 1.2e-180;
Matches 631: Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ATGAATTTGTAAGAGAGATCATTCCTGTATACAAATTTGGTCTGCTACATCA 60
Db 1 ATGAATTTGTAAGAGAGATCATTCCTGTATACAAATTTGGTCTGCTACATCA 60
QY 61 TCGCTGTTGGATGACACCGCTCAGCAAAAGCCGCTGAACCAATCCAGTTGTATG 120
Db 61 TCGCTGTTGGATGACACCGCTCAGCAAAAGCCGCTGAACCAATCCAGTTGTATG 120
QY 121 CACGATATCGAGAGAGCTTCATACAAATTTGGGGAATTAAGAGCTATCTGATCTCAG 180
Db 121 CACGATATCGAGAGAGCTTCATACAAATTTGGGGAATTAAGAGCTATCTGATCTCAG 180
QY 181 GCGTGTACGCGGCGACGCTGTATGCGGTTGATTTGGGACAGACAGGAGCAATTTAT 240
Db 181 GCGTGTACGCGGCGACGCTGTATGCGGTTGATTTGGGACAGACAGGAGCAATTTAT 240
QY 241 AACATGCCCCGGTATTTATCAGATTTGTGCAAAAGTTTAAAGCAAGCGGTCGAAA 300
Db 241 AACATGCCCCGGTATTTATCAGATTTGTGCAAAAGTTTAAAGCAAGCGGTCGAAA 300
QY 301 AAAGTGATTTGTCGCTACAGATTTGGTGGCGGAGACACCTTACTACATAAAAT 360
Db 301 AAAGTGATTTGTCGCTACAGATTTGGTGGCGGAGACACCTTACTACATAAAAT 360
QY 361 CTGACGCGGGAATTAATTTGAAGAGCTGTACGCTTTGGCGGCGAACCCTTGACG 420
Db 361 CTGACGCGGGAATTAATTTGAAGAGCTGTACGCTTTGGCGGCGAACCCTTGACG 420
QY 421 ACAAGCAAGGCGCTCCGGAACAGATCCAAATCAAAAGATTTTATACATCCATTAC 480
Db 421 ACAAGCAAGGCGCTCCGGAACAGATCCAAATCAAAAGATTTTATACATCCATTAC 480
QY 481 AGCAGTCCGATATGATTTGTCATGAATTAATTAAGAGCGGTCTAAACGCT 540
Db 481 AGCAGTCCGATATGATTTGTCATGAATTAATTAAGAGCGGTCTAAACGCT 540
QY 541 CAAATTCATGGCGTTGGGACATTTGTTATGATGAACAGCCAAAGCTGATTT 600
Db 541 CAAATTCATGGCGTTGGGACATTTGTTATGATGAACAGCCAAAGCTGATTT 600
QY 601 AAAGAAGAGCTGAACGCGGCGGCAAAATACGAATTA 639
Db 601 AAAGAAGAGCTGAACGCGGCGGCAAAATACGAATTA 639

RESULT 7
AX418876 639 bp DNA Linear PAT 18-JUN-2002
LOCUS AX418876
DEFINITION Sequence 6 from Patent WO0206457.
ACCESSION AX418876
VERSION AX418876.1 GI:21523731
KEYWORDS
SOURCE Bacillus azotoformans.
ORGANISM Bacillus azotoformans
REFERENCE 1
AUTHORS Giver, L.J., Minshull, J. and Vogel, K.
TITLE Novel Lipase genes
JOURNAL Patent: WO 0206457-A 6 24-JAN-2002;
Maxygen, Inc. (US)
FEATURES Location/Qualifiers

Source	1..639	/organism="Bacillus azotoformans"
BASE COUNT	201 a 121 c 159 g 158 t	
ORIGIN		
Query Match	97.5%; Score 623; DB 6; Length 639;	
Best Local Similarity	98.4%; Pred. No. 1.1e-179;	
Matches 629; Conservative 0; Mismatches 10; Indels 0; Gaps 0;		
OY 1	ATGAATTTGTAAAAAGAGATCATCTGACCTTGTAAACAAATTTTGTCTGTCACTACA 60	
Db 1	ATGAATTTGTAAAAAGAGATCATCTGACCTTGTAAACAAATTTTGTCTGTCACTACA 60	
OY 61	TGCGGTGTGGGATGTCACCGCCGTACAAAAGCCGTGAACACAAATCCAGTTGTATGTT 120	
Db 61	TGCGGTGTGGGATGTCACCGCCGTACAAAAGCCGTGAACACAAATCCAGTTGTATGTT 120	
OY 121	CACGGTATCGAGAGAGCTTCTACAAATTTTGGGAAATTAAGAGCTATCTGTATCTGAG 180	
Db 121	CACGGTATCGAGAGAGCTTCTACAAATTTTGGGAAATTAAGAGCTATCTGTATCTGAG 180	
OY 181	GGCTGCTACCGGGGCAACCTGTATCCGTTGATTTTGGGACAAACAGGAGCAATAT 240	
Db 181	GGCTGCTACCGGGGCAACCTGTATCCGTTGATTTTGGGACAAACAGGAGCAATAT 240	
OY 241	AACATATGCCCGGTATTTATCACGATTTGTGCAAAAGTTTAAAGCAAGCGGTGCGAAA 300	
Db 241	AACATATGCCCGGTATTTATCACGATTTGTGCAAAAGTTTAAAGCAAGCGGTGCGAAA 300	
OY 301	AAAGTGATTTTGTGCTGCACAGTATGSGGTGGCGGCAACACACCTTACTATAAAAAAT 360	
Db 301	AAAGTGATTTTGTGCTGCACAGTATGSGGTGGCGGCAACACACCTTACTATAAAAAAT 360	
OY 361	CTGGACGGCGGAAATTAATTTGAAGAAACGTGCGTGAACGCTGGGGGGCGCAACCGTTCGACG 420	
Db 361	CTGGACGGCGGAAATTAATTTGAAGAAACGTGCGTGAACGCTGGGGGGCGCAACCGTTCGACG 420	
OY 421	ACAAGCAAGGCGCTTCCGGGAAACAGATCCAAATCAAAAGATTTTATACATCATCAATTAC 480	
Db 421	ACAAGCAAGGCGCTTCCGGGAAACAGATCCAAATCAAAAGATTTTATACATCATCAATTAC 480	
OY 481	AGCAGTGGCGATATGATGTGATGAATTAATTAATAATTAAGAGCGGTCTAAAAACCT 540	
Db 481	AGCAGTGGCGATATGATGTGATGAATTAATTAATAATTAAGAGCGGTCTAAAAACCT 540	
OY 541	CAAAATTCATGGCGTTGGGACATGCTGTTTATGATGAAGACGCAAGTCAACAGCTGATT 600	
Db 541	CAAAATTCATGGCGTTGGGACATGCTGTTTATGATGAAGACGCAAGTCAACAGCTGATT 600	
OY 601	AAAGAGAGCATGAAACGCGGGGGCCAAAATACGAATTAA 639	
Db 601	AAAGAGAGCATGAAACGCGGGGGCCCTAATACAAAATTAA 639	
RESULT 8		
AX418873		
LOCUS	AX418873	
DEFINITION	Sequence 3 from Patent WO0206457.	
ACCESSION	AX418873	
VERSION	AX418873.1	
KEYWORDS	GI:21523728	
SOURCE		
ORGANISM	Bacillus megaterium.	
REFERENCE	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	
AUTHORS	Glover, L.J., Minshull, J. and Vogel, K.	
TITLE	Novel lipase genes	
JOURNAL	Patent: WO 0206457-A 3 24-JAN-2002;	
FEATURES	Maxygen, Inc. (US)	
Source	Location/Qualifiers	
	1..639	
	/organism="Bacillus megaterium"	

BASE COUNT	200 a	122 c	158 g	159 t
ORIGIN	/db_xref="taxon:1404"			
Query Match	94.9%; Score 606.4; DB 6; Length 639;			
Best Local Similarity	98.8%; Pred. No. 1.4e-174;			
Matches 632; Conservative	0; Mismatches 6; Indels 2; Gaps 2;			

OY	1	ATGAATTGTTAAAAAGAAAGATCATTCGTACCTTGTAACAATTTTGGTGTGCATGCACA	60
Db	1	ATGAAATTTGTTTTAAAAGAAGATCATTCGTACTGTAAACAATTTTGGTGTGCATGCACA	60
OY	61	TCCGTGTTTGGATGCAACCCTCAGCAAACCCCGTGAACACAAATCCAGTTGTATGTT	120
Db	61	TCCGTGTTTGGATGCAACCCTCAGCAAACCCCGTGAACACAAATCCAGTTGTATGTT	119
OY	121	CAC-GGTATCGGAGAGCTCATACAAATTTTGGGGAATTAAGAGCTATCTCGATATCCA	179
Db	120	CACGTGTATCCGAGAGAGCTCATACAAATTTTGGGGAATTAAGAGCTATCTCGATATCCA	179
OY	180	GGGGTGGTCACGGGGCAACGTGTATGGGTGATTTTGGGCAAGACAGGAGCAATTA	239
Db	180	GGGGTGGTCACGGGGCAACGTGTATGGGTGATTTTGGGCAAGACAGGAGCAATTA	239
OY	240	TAACAATGGCCCCGGTATTATCACGATTTTGTCMAAAGGTTTTAGACGAAGCGGTGC	299
Db	240	TAACAATGGCCCCGGTATTATCACGATTTTGTCMAAAGGTTTTAGACGAAGCGGTGC	299
OY	300	AAAAGTGGATTTTGTTCGTCTACAGTATGGTGGGCCGAACACACCTTACTACATAAAAA	359
Db	300	AAAAGTGGATTTTGTTCGTCTACAGATGCGTGGGCCGAACACACTTACTACATAAAAA	359
OY	360	TCTGGACGGCGGAATATAAATTGAAGAACGTGTACGCTTGGCGCGGAACCGTTGCAC	419
Db	360	TCTGGACGGCGGAATATAAATTGAAGAACGTGTACGCTTGGCGCGGAACCGTTGCAC	419
OY	420	GACAAGCAGGCGCTTCGGGACACAGATCCAAATCAAAAGATTTTATACATCCATTTA	479
Db	420	GACAAGCAGGCGCTTCGGGACACAGATCCAAATCAAAAGATTTTATACATCCATTTA	479
OY	480	CAGAGTGCCCATTTGATTTGATGAATTTACTTATCAAAATAGACGGTGGTAAAAAGC	539
Db	480	CAGAGTGCCCATTTGATTTGATGAATTTACTTATCAAAATAGACGGTGGTAAAAAGC	539
OY	540	TCAATTCATGCGCTTGGGACATTTGTTTATGTAAGAACGCCAAGTCAAGAGCCTGAT	599
Db	540	TCAATTCATGCGCTTGGGACATTTGTTTATGTAAGAACGCCAAGTCAAGAGCCTGAT	599
OY	600	TAAAGAGGACTGAAGCGCGGGGCGCAAAATATGCAATTA	639
Db	600	TAAAGAGGACTGAAGCGCGGGGCGCAAAATATGCAATTA	639

RESULT 9	AB000617	35000 bp	DNA	linear	BCT 12-SEP-1997
LOCUS	AB000617				
DEFINITION	Bacillus subtilis genomic DNA, 22 to 25 degree region, complete cds.				
ACCESSION	AB000617				
VERSION	AB000617.1	GI:2415716			
KEYWORDS	yack; NaB; yceG; ycek; ycej; ycel; yceH; ycef; ycee; yced; ycec; yceb; ycdA; ycdI; ycdH; ycdG; ycdf; RapD; ycdJ; ycdK; ycdB; ycdA; Neta; yceH; yccS; yccF; ycce; yccc; yccb; Trlacylglycerol lipase; LmrA; ycea; LmrP; ycbU.				
SOURCE	Bacillus subtilis (strain:168 trpC2) DNA.				
ORGANISM	Bacillus subtilis				
REFERENCE	1 (sites)				
AUTHORS	Kumano,M., Tamakoshi,A. and Yamane,K.				
TITLE	A 32 kb nucleotide sequence from the region of the lincomycin-resistance gene (22-25 degree) of the Bacillus subtilis chromosome and identification of the site of the lin-2 mutation				
JOURNAL	Unpublished				

REFERENCE 2 (bases 1 to 35000)
AUTHORS Yamane,K.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-1997) Kunio Yamane, University of Tsukuba,
Institute of Biological Sciences: 1-1-1 Ten-ohda, Tsukuba, Ibaraki
305, Japan (Tel:0298-53-6680, Fax:0298-53-6680)
FEATURES
Source Location/Qualifiers
1. .35000
/organism="Bacillus subtilis"
/strain="168 trpc2"
/db_xref="taxon:1423"
/map="22 to 25 degree"
592. .1704
/gene="ycbU"
592. .1704
/gene="ycbU"
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pyridoxal-phosphate-dependent aminotransferase"
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/protein_id="BAA22227.1"
/db_xref="GI:2415717"
/translation="MEHLPEYROLPEPTLQTHMLASCSALAEPSRAIODYDSTL
LYKTNKKEAIKTEFARNFPAKIGNEPPEVAIVPSVSDALVSASYLTAIFGKHVY
YTDMPFAPHVWQHSIDYVSIPSIDGLPLEQETHISDETVLTCVPHVHRDXY
VODIKAJELISQKSGSLLEVDAYOSAGHPIIDVKEWVDMLAAGTRKYLIGIPVAL
YVRKELADALPKRASAMFGRESGDGAIVAKVARRFGTPTAFISVAAAALSLNHI
GVSHIRDHVKTICADAVOYAAEKGILQAAAGGIOPGMAVIRDERASETGLKKRY
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complement(1746. .3185)
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complement(1746. .3185)
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/note="lincomycin-resistance protein, similar to
multidrug-resistant protein
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/codon_start=1
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/protein_id="BAA22228.1"
/db_xref="GI:2415718"
/translation="MIUETAKASQOYKVPIMISILLAGFIMSEFALNATLIDLM
KEINTATVOMLTGGLYGLIVPGSILGPIRQTLPTVSLFSLTCTPAAAL
PSFSLAARIQVAGLGLPLMFNTLIVTFPPHKGAMGTIGLIVMPRAPIGPF
SGVLELNMHWIWMISLPVLVAVGLIAMOVSETPKPIDVLSIILSTIGGFI
VFESNAGSGSSPTVIVSLIVGVGLFESIRQITKOPMNLARFYPMFLIG
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RESULT 10
BSUB0002
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
1 (bases 1 to 221160)
Kunst, F., Ogasawara, N., Moszer, I., Albertini, A.M., Allion, G.,
Azevedo, V., Bertoletti, M.G., Bessieres, P., Bolotin, A., Borcher, S.,
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Danchin, A.

The complete genome sequence of the gram-positive bacterium
Bacillus subtilis
Nature 390 (6657), 249-256 (1997)
98044033
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2 (bases 1 to 221160)
Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.
Direct Submission
Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur,
Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 75724
Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr,
adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45
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FEATURES
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terminator				
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DEFINITION	A02815	Artificial gene for lipase comprising HindIII-EcoRI segment.	
VERSION	A02815.1	GI:412317	
KEYWORDS	lipase.		
SOURCE	synthetic construct.		
ORGANISM	synthetic construct.		
REFERENCE	1 (bases 1 to 1831)		
AUTHORS	Vandamme,E., Schanck-Brodbeck,K.H., Colson,C. and Hanotier,J.D.V.		
TITLE	DNA segment coding for a specific lipase, vectors for the expression thereof, microorganisms transformed by these vectors and use of these microorganisms for the production of the lipase		
JOURNAL	Patent: EP 0243338-A 3 28-OCT-1987;		
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ORIGIN			
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Db	503	AAAGTGATATTGTGCGTCGACGATGGGGGCGCAACACACTTTACTACATAAAAT	562
QY	301	AAAGTGATATTGTGCGTCACAGTATGGGTGGCGCAACACACTTACTACATAAAAT	360
Db	563	AAAGTGATATTGTGCGTCGCGTCGACGATGGGGGCGCAACACACTTACTACATAAAAT	360
QY	361	CTGGACGGCGGGAATAAATTGAANAACGCTGAAGCTGGGGGGCGCAACCGTTCGACG	420
Db	563	CTGGACGGCGGGAATAAATTGAANAACGCTGCGACGCTGGGGGGCGCAACCGTTCGACG	420

OY	421	ACAACGAGCGCCCTTCGGGAACACATGCCAATTCAAAAGATTTTATACACATCCATTAC	480
Dd	623	ACAGGCAGAAGGCGCTTCCGGGAACACATCCAAATCAAAGATTTTATACACATCCATTAC	682
OY	481	ACCAGTGGCGATATATGTGTCAATTAATCTATCAAAAATTAAGACGGTGCTAAAAAGCCT	540
Dd	683	ACCATGTCCGATATATGTGTCAATTAATCTATCAAAAATTAAGATGTGTGTGTAAGAACGTT	742
OY	541	CAAAATTCATGGCGTTGGGCACATTTGGTTTTATGATGAACAGCCAAAGTCACAGCGCTGATT	600
Dd	743	CAAAATTCATGGCGTTGGGCACATTCGCGCTTGTGTACACAGCCAAAGTCACAGCGCTGATT	802
OY	601	AAAGAAGACTGAACGGCGGGGGGCAAAATACGATTTAA	639
Dd	803	AAAGAAGGGGTGAACGGCGGGGGCCAAGATTCGAATTTAA	841
RESULT 14			
LOCUS	A02816/c	A02816	1831 bp DNA linear PAT 16-JUN-1993
DEFINITION		Artificial sequence comprising HindIII-EcoRI segment, reverse complement.	
ACCESSION		A02816	
VERSION		A02816.1	GI:410908
KEYWORDS			
SOURCE			
ORGANISM		synthetic construct.	
REFERENCE		synthetic construct.	
AUTHORS		artificial sequences.	
TITLE		1 (bases 1 to 1831)	
JOURNAL		Vandamme,E., Schanck-Brodrueck,K.H., Colson,C. and Hanotier,J.D.V. DNA segment coding for a specific lipase, vectors for the expression thereof, microorganisms transformed by these vectors and use of these microorganisms for the production of the lipase Patent: EP 0243338-A 4 28-Oct-1987; FINA RESEARCH S.A	
FEATURES			
source		Location/Qualifiers	
		1..1831	
BASE COUNT		/organism="synthetic construct"	
ORIGIN		/db_xref="taxon:32630"	
		463 a 416 c 367 g 585 t	
Query Match		88.5%; Score 565.4; DB 6; Length 1831;	
Best Local Similarity		92.8%; Pred. No. 6.2e-162;	
Matches 593; Conservative 0; Mismatches 46; Indels 0; Gaps 0;			
OY	1	ATGAATAATTTGTA AAAAGAAGATCATTCGATTCACATTTTGGTCTGTCATGTACA	60
Dd	1629	ATGAATAATTTGTA AAAAGAAGATCATTCGATTCACATTTTGGTCTGTCATGTACA	1570
OY	61	TGCGTGTTTGGCATCGACCGCTGACAAAAGCCGCTGAACACATCCAGTTTATGGTT	120
Dd	1569	TGCGTGTTTGGCATTCACCGCTGACAAAAGCCGCTGAACACATCCAGTTTATGGTT	1510
OY	121	CACGGTATCGAGAGAGCTTCATACATTTTGGGGGAATTAAGACTATCTGATCTCAG	180
Dd	1509	CACGGTATTTGGAGGGGACACATTCATTTTGGGGGAATTAAGAGCTATCCGATCTCAG	1450
OY	181	GCGTGTCACGGGGCAAGCTGTATCGGGTTGATTTTGGGACAAAGACAGGAGCAATTTAT	240
Dd	1449	GCGTGTCGCGGGCAACACTGTATCGAGTTGATTTTGGGACAAAGACAGGCAAAATTTAT	1390
OY	241	AACATATGCCCCGCTATTATTCACGATTTTGTGCAAAAAGTTTATAGACGAAAGGGTGCGAAA	300
Dd	1389	AACATATGACCGGATTTATTCGCGATTTTGTGCAAAAAGTTTATAGATGAACGGTGCGAAA	1330
OY	301	AAAGTGATATTGTGCTCACAGTATGGGTGGCGGGAACACACTTACTATCAATAAAAT	360
Dd	1329	AAAGTGATATTGTGCTGCGACAGCATGGGGGGCGGGAACACACTTACTATCAATAAAAT	1270
OY	361	CTGGACGGCGGAATTAATAATGAAGAGCTGTAACGCTTTGGGGCGGCAACCGTTGCAGC	420

Db	1269	CTGGACGGGGGAAATAAAGTTGCAAAACGTCGTGACGCTTGGGGGGCGGCAACCGTTTGACG	1210
QY	421	ACAACGACGGCGCTTCGGGAAACAGATCCAAATCAAAAGATTTTATACACATCCATTTAC	480
Db	1209	ACAGGCAAGGGCGCTTCGGGAAACAGATCCAAATCAAAAGATTTTATACACATCCATTTAC	1150
QY	481	ACGACGTGCGGATATATTTGTCATGAATTAATCTATCAAAATTAAGACGGTGTCAAAAAGCT	540
Db	1149	AGCACTGCCGATATATTTGTCATGAATTAATCTATCAAAATTAAGATGTGTCTAGAAAGCTT	1090
QY	541	CAAAATTCATGCGCGTTGGGCACATTGGTTTATGTATGAACAGCCCAAGTCACAGCCTGATT	600
Db	1089	CAAAATTCATGCGCGTTGGGCACATCCGCGCTTGTGTACACAGCCCAAGTCACAGCCTGATT	1030
QY	601	AAAGAAGCACTGAACGGCGGGGGCCAAAATATGCAATTA	639
Db	1029	AAAGAAGGGCTGAACGGCGGGGCGCAAGATTAAGATTA	991
RESULT	15		
LOCUS	AX418872	639 bp	DNA
DEFINITION	AX418872	Sequence 2 from Patent WO0206457.	Linear
ACCESSION	AX418872		PAT 18-JUN-2002
VERSION	AX418872.1	GI:21523727	
KEYWORDS			
SOURCE			
ORGANISM	Bacillus subtilis.		
REFERENCE	1	Bacillus subtilis.	
AUTHORS	Glier, L.J., Minshull, J. and Vogel, K.	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	
TITLE	Novel lipase genes		
JOURNAL	Patent: WO 0206457-A 2 24-JAN-2002;		
FEATURES	Maxygen, Inc. (US)		
Source	1. 639	Location/Qualifiers	
BASE COUNT	194 a	/organism="Bacillus subtilis"	
ORIGIN	126 c	/db_xref="taxon:1423"	
	161 g		
	158 t		
Query Match	88.3%	Score 564.4; DB 6; Length 639;	
Best Local Similarity	92.8%;	Pred. No. 1e-161;	
Matches	592; Conservative	0; Mismatches 46; Indels 0; Gaps 0;	
QY	1	ATGAATTTGTAAAGAAGATCATTCACCTTGAACAATTTTGTGCTGTCAGTCACA	60
Db	1	ATGAATTTGTAAAGAAGATCATTCACCTTGAACAATTTTGTGCTGTCAGTCACA	60
QY	61	TGCGTGTTCGCGATGCGACCGCGTCAGCAAAAGCCGCTGAACACATCATCGTTTATGAGTTT	120
Db	61	TGCGTGTTCGCGATGCGACCGCGTCAGCAAAAGCCGCTGAACACATCATCGTTTATGAGTTT	120
QY	121	CACGGTATTCGCGAGCGCTTATACAAATTTGGGGAAATTAAGAGCTATCTGTAATTCAG	180
Db	121	CACGGTATTCGCGAGCGCATTCATCAATTTTGGGGAAATTAAGAGCTATCTGTAATTCAG	180
QY	181	GGCTGTGTCAGGGGCAAGCTGTATGCGGTTGATTTTGGGCAAGACAGGAGCAATTTAT	240
Db	181	GGCTGTGTCAGGGGCAAGCTGTATGCGGTTGATTTTGGGCAAGACAGCAAAATTTAT	240
QY	241	AACATATGCGCCGGTATTTATCAACGATTTTGTGCAAAAGTTTATAGCAAAAGCGGTGCGAAA	300
Db	241	AACATATGCGCGATTTATCAACGATTTTGTGCAAAAGTTTATAGCAAAAGCGGTGCGAAA	300
QY	301	AAAGTGATATTTGTCGTACACAGTATGGGTGGCGGCAACACACCTTACTATCAATAAAAAAT	360
Db	301	AAAGTGATATTTGTCGTACACAGTATGGGGGGCGGGAACACACCTTACTATCAATAAAAAAT	360
QY	361	CTGGACGGCGGGAATTAATTAAGACGTCGTACGCTTGGCGGGCGGCAACCGTTTCAGC	420
Db	361	CTGGACGGCGGGAATTAAGACGTCGTGAGAGCTTGGCGGGCGGCAACCGTTTTCAGC	420

DR WPI: 2002-171805/22.
 DR P-PSDB: AAU83841.
 PT Nucleic acids encoding lipase enzymes which are useful as supplements
 PT in animal feeds, as agents of flavour modification and for treating
 PT Crohn's disease and coeliac disease -
 XX
 PS Claim 81; Page 117; 196pp; English.
 XX
 CC The invention relates to new *Bacillus* lipase enzymes and the nucleic
 CC acids encoding them. The lipase polypeptides are useful as supplements in
 CC animal feeds, as agents of flavour modification and fat modification in
 CC human foodstuffs (e.g. cheese), as agents in the creation of food
 CC emulsifiers, as agents for tanning/processing of leather and as cleaning
 CC agents. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences ABK3819-ABK3874 represent *Bacillus* lipase
 CC polynucleotides of the invention.
 XX

SQ Sequence 639 BP; 201 A; 123 C; 159 G; 156 T; 0 other:

Query Match 100.0%; Score 639; DB 24; Length 639;
 Best Local Similarity 100.0%; Pred. No. 4.2e-190;
 Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAATTTGTAAGAGAGATTCATTCGATTAACATTTTGGCTGTCAGTCACA 60
 DB 1 ATGAAATTTGTAAGAGAGATTCATTCGATTAACATTTTGGCTGTCAGTCACA 60
 QY 61 TCGCTGTTGGATGACAGCCCTGACAGAAAGCCGCTGAACACATCATGTTATGCTT 120
 DB 61 TCGCTGTTGGATGACAGCCCTGACAGAAAGCCGCTGAACACATCATGTTATGCTT 120
 QY 121 CACGATATCGAGAGAGCTTACATTAATTTGCGGAATTAAGAGCTATCTGATCTCAG 180
 DB 121 CACGATATCGAGAGAGCTTACATTAATTTGCGGAATTAAGAGCTATCTGATCTCAG 180
 QY 181 GCGTGTACAGCGGCAAGCTGTATGCTTATTTGGCAAGACAGAGCAATTTAT 240
 DB 181 GCGTGTACAGCGGCAAGCTGTATGCTTATTTGGCAAGACAGAGCAATTTAT 240
 QY 241 AACAAATGCGCGGTATATACAGATTTGTGCAAAAGTTTAAAGCAAAAGCGGTGCGAAA 300
 DB 241 AACAAATGCGCGGTATATACAGATTTGTGCAAAAGTTTAAAGCAAAAGCGGTGCGAAA 300
 QY 301 AAAGTGATATGTCGCTACAGATATGGTGGCGGAACACACCTTACTACATAAAAT 360
 DB 301 AAAGTGATATGTCGCTACAGATATGGTGGCGGAACACACCTTACTACATAAAAT 360
 QY 361 CTGAGACGCGGAATTAATTTGAAACACGTCGTAACGCTTGCGGCGCAACGCTTGACG 420
 DB 361 CTGAGACGCGGAATTAATTTGAAACACGTCGTAACGCTTGCGGCGCAACGCTTGACG 420
 QY 421 ACAAGCAAGCGGCTTCCGGGAACAGATCCAAATCAAAAGATTTTATACATTCATTTAC 480
 DB 421 ACAAGCAAGCGGCTTCCGGGAACAGATCCAAATCAAAAGATTTTATACATTCATTTAC 480
 QY 481 AGCAGTGGCGATATGATTTGTCATGAATTTACTTATCAAAATTTAGACGGTCTAAAAACGCT 540
 DB 481 AGCAGTGGCGATATGATTTGTCATGAATTTACTTATCAAAATTTAGACGGTCTAAAAACGCT 540
 QY 541 CAATTCATGCGCTTGGGACATTTGTTTATTTGATGAACAGCAAGTCAACAGCCTGATT 600
 DB 541 CAATTCATGCGCTTGGGACATTTGTTTATTTGATGAACAGCAAGTCAACAGCCTGATT 600
 QY 601 AAAGAGAGCTGAACGCGGCGGCGCAAAATACGAATTA 639
 DB 601 AAAGAGAGCTGAACGCGGCGGCGCAAAATACGAATTA 639

RESULT 2

ABK3825
 ID ABK3825 standard; DNA; 639 BP.
 XX
 AC ABK3825;
 DT 08-MAY-2002 (first entry)
 XX
 DE *Bacillus* lipase polynucleotide #7.
 XX
 KW Lipase; *Bacillus*; animal feed; flavour modification; fat modification;
 KW human foodstuff; cheese; food emulsifier; leather tanning; gene; ds;
 KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
 KW gastroenteric; anti-inflammatory; respiratory;
 KW gastroenteric.
 XX
 OS *Bacillus* firmus.
 XX
 PN MO200206457-A2.
 XX
 PD 24-JAN-2002.
 XX
 PE 13-JUL-2001; 2001MO-US22160.
 XX
 PR 13-JUL-2000; 2000US-217954P.
 PR 21-JUN-2001; 2001US-300378P.
 XX
 PA (MAXY-) MAXYGEN INC.
 XX
 PI Glyser LJ, Minshull J, Vogel K;
 XX
 DR WPI: 2002-171805/22.
 DR P-PSDB: AAU83841.
 PT Nucleic acids encoding lipase enzymes which are useful as supplements
 PT in animal feeds, as agents of flavour modification and for treating
 PT Crohn's disease and coeliac disease -
 XX
 PS Claim 81; Page 119-120; 196pp; English.
 XX
 CC The invention relates to new *Bacillus* lipase enzymes and the nucleic
 CC acids encoding them. The lipase polypeptides are useful as supplements in
 CC animal feeds, as agents of flavour modification and fat modification in
 CC human foodstuffs (e.g. cheese), as agents in the creation of food
 CC emulsifiers, as agents for tanning/processing of leather and as cleaning
 CC agents. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences ABK3819-ABK3874 represent *Bacillus* lipase
 CC polynucleotides of the invention.
 XX
 SQ Sequence 639 BP; 202 A; 123 C; 157 G; 157 T; 0 other:

Query Match 98.5%; Score 629.4; DB 24; Length 639;
 Best Local Similarity 99.1%; Pred. No. 4.3e-187;
 Matches 633; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGAAATTTGTAAGAGAGATTCATTCGATTAACATTTTGGCTGTCAGTCACA 60
 DB 1 ATGAAATTTGTAAGAGAGATTCATTCGATTAACATTTTGGCTGTCAGTCACA 60
 QY 61 TCGCTGTTGGATGACAGCCCTGACAGAAAGCCGCTGAACACATCATGTTATGCTT 120
 DB 61 TCGCTGTTGGATGACAGCCCTGACAGAAAGCCGCTGAACACATCATGTTATGCTT 120
 QY 121 CACGATATCGAGAGAGCTTACATTAATTTGCGGAATTAAGAGCTATCTGATCTCAG 180
 DB 121 CACGATATCGAGAGAGCTTACATTAATTTGCGGAATTAAGAGCTATCTGATCTCAG 180

QY 181 GGCTGTCACGGGCAAGCTGTATCGGTTGATTTTGGGACAGACAGCAATTTAT 240
DB 181 GGCTGTCACGGGCAAGCTGTATCGGTTGATTTTGGGACAGACAGCAATTTAT 240
QY 241 AACAAATGCGCGGTATATACAGATTTTGTCAAAAGTTTATAGCAAAACGGGTCGAAA 300
DB 241 AACAAATGCGCGGTATATACAGATTTTGTCAAAAGTTTATAGCAAAACGGGTCGAAA 300
QY 301 AAAGTGATTTGTGCTTCACAGTATGGTGGCGGACACACCTTACATCAATTTAAC 360
DB 301 AAAGTGATTTGTGCTTCACAGTATGGTGGCGGACACACCTTACATCAATTTAAC 360
QY 361 CTGACGCGCGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
DB 361 CTGACGCGCGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
QY 421 ACAAGCAAGGCGCTTCGCGGAACAGATCCAAATCAAAATTTATACATTCATTTAC 480
DB 421 ACAAGCAAGGCGCTTCGCGGAACAGATCCAAATCAAAATTTATACATTCATTTAC 480
QY 481 AGCAGTGGCGATATGATTTGTCAATTAATTAATTAATTAATTAATTAATTAAT 540
DB 481 AGCAGTGGCGATATGATTTGTCAATTAATTAATTAATTAATTAATTAATTAAT 540
QY 541 CAAATTCATGCGGTGGGACATTTGTTATGATGAACAGCAAGTCAACAGCGCTGAT 600
DB 541 CAAATTCATGCGGTGGGACATTTGTTATGATGAACAGCAAGTCAACAGCGCTGAT 600
QY 601 AAAGAAGACGTGAAACGGCGGAGCCCAATACAAATTTAA 639
DB 601 AAAGAAGACGTGAAACGGCGGAGCCCAATACAAATTTAA 639

RESULT 3

ABK33826
ID ABK33826 standard; DNA: 639 BP.

XX AC ABK33826;

XX DT 08-MAY-2002 (first entry)

XX DE Bacillus lipase polynucleotide #8.

XX KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; gene; ds;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
KW gastrointestinal.

XX KW Bacillus badius.

XX OS WO200206457-A2.

XX PN 24-JAN-2002.

XX PD 13-JUL-2001; 2001WO-US22160.

XX PF 13-JUL-2001; 2000US-217954P.

XX PR 21-JUN-2001; 2001US-300378P.

XX PA (MAXY-) MAXYGEN INC.

XX PI Giver LJ, Minshull J, Vogel K;

XX DR WPI: 2002-171805/22.

XX P-PSDB: AA083848.

XX PT Nucleic acids encoding lipase enzymes which are useful as supplements
XX in animal feeds, as agents of flavour modification and for treating
XX Crohn's disease and coeliac disease -

PS Claim 81; Page 120; 196pp; English.

CC The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences ABK33819-ABK33874 represent Bacillus lipase
CC polynucleotides of the invention.

XX SQ Sequence 639 BP; 202 A; 122 C; 157 G; 158 T; 0 other;

Query Match 98.2%; Score 627.8; DB 24; Length 639;

Best Local Similarity: 98.9%; Pred. No. 1.4e-186;

Matches 632; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGAATTTGTAAAAAGAGATCATTCGACCTTGTAAACATTTTGGTGTGCTGACAC 60
DB 1 ATGAATTTGTAAAAAGAGATCATTCGACCTTGTAAACATTTTGGTGTGCTGACAC 60
QY 61 TCGCTGTTGGCATGACGCGGTGACGAAAGCGCGTGAACAAATTCAGTTTATGCTT 120
DB 61 TCGCTGTTGGCATGACGCGGTGACGAAAGCGCGTGAACAAATTCAGTTTATGCTT 120
QY 121 CACGGTATCGAGGAGAGCTTCATACATTTTGGGGAATTTAAGCTATCTGATCTCAG 180
DB 121 CACGGTATCGAGGAGAGCTTCATACATTTTGGGGAATTTAAGCTATCTGATCTCAG 180
QY 181 GGCTGTCACGGGCAAGCTGTATCGGTTGATTTTGGGACAAACAGCAATTTAT 240
DB 181 GGCTGTCACGGGCAAGCTGTATCGGTTGATTTTGGGACAAACAGCAATTTAT 240
QY 241 AACAAATGCGCGGTATATACAGATTTTGTCAAAAGTTTATAGCAAAACGGGTCGAAA 300
DB 241 AACAAATGCGCGGTATATACAGATTTTGTCAAAAGTTTATAGCAAAACGGGTCGAAA 300
QY 301 AAAGTGATTTGTGCTTCACAGTATGGTGGCGGACACACCTTACATCAATTTAAC 360
DB 301 AAAGTGATTTGTGCTTCACAGTATGGTGGCGGACACACCTTACATCAATTTAAC 360
QY 361 CTGACGCGCGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
DB 361 CTGACGCGCGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
QY 421 ACAAGCAAGGCGCTTCGCGGAACAGATCCAAATCAAAATTTATACATTCATTTAC 480
DB 421 ACAAGCAAGGCGCTTCGCGGAACAGATCCAAATCAAAATTTATACATTCATTTAC 480
QY 481 AGCAGTGGCGATATGATTTGTCAATTAATTAATTAATTAATTAATTAATTAAT 540
DB 481 AGCAGTGGCGATATGATTTGTCAATTAATTAATTAATTAATTAATTAATTAAT 540
QY 541 CAAATTCATGCGGTGGGACATTTGTTATGATGAACAGCAAGTCAACAGCGCTGAT 600
DB 541 CAAATTCATGCGGTGGGACATTTGTTATGATGAACAGCAAGTCAACAGCGCTGAT 600
QY 601 AAAGAAGACGTGAAACGGCGGAGCCCAATACAAATTTAA 639
DB 601 AAAGAAGACGTGAAACGGCGGAGCCCAATACAAATTTAA 639

RESULT 4

ABK33822
ID ABK33822 standard; DNA: 639 BP.

XX AC ABK33822;

DT 08-MAY-2002 (first entry)
XX
DE Bacillus lipase polynucleotide #4.
XX
KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; gene; ds;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; anti-inflammatory; respiratory;
XX
XX Bacillus lentus.
XX
PN W0200206457-A2.
XX
PD 24-JAN-2002.
XX
PF 13-JUL-2001; 2001MO-US22160.
XX
PR 13-JUL-2000; 2000US-217954P.
PR 21-JUN-2001; 2001US-300378P.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Giver LJ, Minshull J, Vogel K;
XX
DR WPI: 2002-171805/22.
DR P-PSDB; AAU83844.
XX
PT Nucleic acids encoding lipase enzymes which are useful as supplements
PT in animal feeds, as agents of flavour modification and for treating
PT Crohn's disease and coeliac disease -
XX
PS Claim 81; Page 118; 196pp; English.
XX
CC The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences ABK33819-ABK33874 represent Bacillus lipase
CC polynucleotides of the invention.
XX
SQ Sequence 639 BP; 203 A; 120 C; 157 G; 159 T; 0 other;
Query Match 98.0%; Score 626.2; DB 24; Length 639;
Best Local Similarity 98.7%; Pred. No. 4,3e-186;
Matches 631; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 ATGAAATTTGTAAGAGAGATCATTCGACTTGTAAATTTGGTCTGCTCA 60
DB 1 ATGAAATTTGTAAGAGAGATCATTCGACTTGTAAATTTGGTCTGCTCA 60
QY 1 TCAGTGTTCGATGACGCGTCAAGCAAAACCGCTGCAACATCCGTTGTTATG 120
DB 1 TCAGTGTTCGATGACGCGTCAAGCAAAACCGCTGCAACATCCGTTGTTATG 120
QY 121 CACGATATCGAGAGAGCTTATACATTTTCGGGAATTAAGAGCTATCTGATCTCAG 180
DB 121 CACGATATCGAGAGAGCTTATACATTTTCGGGAATTAAGAGCTATCTGATCTCAG 180
QY 181 GCGTGTACGCGGAGAGCTATGCGGTATTTTGGCAACAGACGGAGCAATAT 240
DB 181 GCGTGTACGCGGAGAGCTATGCGGTATTTTGGCAACAGACGGAGCAATAT 240
QY 241 AACATGCGCGGTATTCAGATTTGTGCAAAAGTTTACAGAAACGGGTCCGAA 300
DB 241 AACATGCGCGGTATTCAGATTTGTGCAAAAGTTTACAGAAACGGGTCCGAA 300

DB 241 AACATGCGCGGTATTCAGATTTGTGCAAAAGTTTACAGAAACGGGTCCGAA 300
QY 301 AAGTGTATTTGTCGCTACAGATATGAGTGCGCGCAACACCTTACTATATAAAAT 360
DB 301 AAGTGTATTTGTCGCTACAGATATGAGTGCGCGCAACACCTTACTATATAAAAT 360
QY 361 CTGAGCGCGGAAATTAATTAAGAAACGTCGTAAACGCTTGGCGCGCAACGTTGACG 420
DB 361 CTGAGCGCGGAAATTAATTAAGAAACGTCGTAAACGCTTGGCGCGCAACGTTGACG 420
QY 421 ACAAGCAAGCGGCTCCGGGACAGATCCAAATCAAAAGTTTATACATCCATTC 480
DB 421 ACAAGCAAGCGGCTCCGGGACAGATCCAAATCAAAAGTTTATACATCCATTC 480
QY 481 AGCAGTCCGATATGATTCATGATTAATTAATTAAGAGCGTGTAAACGCT 540
DB 481 AGCAGTCCGATATGATTCATGATTAATTAATTAAGAGCGTGTAAACGCT 540
QY 541 CAAATTCATGCGGCTTGGGACATTTGTTATGTAAGACCAAGTCAACAGCTGATT 600
DB 541 CAAATTCATGCGGCTTGGGACATTTGTTATGTAAGACCAAGTCAACAGCTGATT 600
QY 601 AAGAGGACTGAAAGCGGCGGCAATTAATCAATTA 639
DB 601 AAGAGGACTGAAAGCGGCGGCAATTAATCAATTA 639
RESULT 5
ABK33823
ID ABK33823 standard; DNA: 639 BP.
XX
AC ABK33823;
XX
DT 08-MAY-2002 (first entry)
XX
DE Bacillus lipase polynucleotide #5.
XX
KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; gene; ds;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; anti-inflammatory; respiratory;
XX
XX Bacillus circulans.
XX
OS W0200206457-A2.
XX
PN W0200206457-A2.
XX
PD 24-JAN-2002.
XX
PF 13-JUL-2001; 2001MO-US22160.
XX
PR 13-JUL-2000; 2000US-217954P.
PR 21-JUN-2001; 2001US-300378P.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Giver LJ, Minshull J, Vogel K;
XX
DR WPI: 2002-171805/22.
DR P-PSDB; AAU83845.
XX
PT Nucleic acids encoding lipase enzymes which are useful as supplements
PT in animal feeds, as agents of flavour modification and for treating
PT Crohn's disease and coeliac disease -
XX
PS Claim 81; Page 118-119; 196pp; English.
XX
CC The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning

CC agents. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences ABK3819-ABK3874 represent *Bacillus lipase*
 CC polynucleotides of the invention.

XX Sequence 639 BP; 201 A; 122 C; 157 G; 159 T; 0 other;

Query Match 98.0%; Score 626.2; DB 24; Length 639;
 Best Local Similarity 98.7%; Pred. No. 4.3e-186;
 Matches 631; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 ATGAATTTGTAAGAAAGATCATGCACTTGTACAAATTTGGTGTGACAGCACA 60
 DB 1 ATGAATTTTATAAGAAAGATCATGCACTTGTACAAATTTGGTGTGACAGCACA 60
 OY 61 TCGCTGTTTGCATGACGCGCTCAGCAAAAGCCGCTGAACACATTCAGTTGTATGTT 120
 DB 61 TCGCTGTTTGCATGACGCGCTCAGCAAAAGCCGCTGAACACATTCAGTTGTATGTT 120
 OY 121 CACGGTATCGAGAGCTTCATACAAATTTGGGGAATTAAGAGCTATCTCTATCTCAG 180
 DB 121 CACGGTATCGAGAGCTTCATACAAATTTGGGGAATTAAGAGCTATCTCTATCTCAG 180
 OY 181 GGCTGTACGGGGGAGAGCTGTATGCGTTTGGGACACAGGAGCGAATTT 240
 DB 181 GGCTGTACGGGGGAGAGCTGTATGCGTTTGGGACACAGGAGCGAATTT 240
 OY 241 AACCAATGCGCCGCTATTTACAGATTTTGCAAAAGGTTTGTAGAGCAAAAGCGGTGCGA 300
 DB 241 AACCAATGCGCCGCTATTTACAGATTTTGCAAAAGGTTTGTAGAGCAAAAGCGGTGCGA 300
 OY 301 AAAGTGAATTTGTGCTCAGATTTGGTGGCGGACACACCTTACTACATAAAAT 360
 DB 301 AAAGTGAATTTGTGCTCAGATTTGGTGGCGGACACACCTTACTACATAAAAT 360
 OY 361 CTGAGCGGCGGAAATTAATTAAGAAAGCTGTACGCTTGGGCGGCGAAGCGTTGCGAG 420
 DB 361 CTGAGCGGCGGAAATTAATTAAGAAAGCTGTACGCTTGGGCGGCGAAGCGTTGCGAG 420
 OY 421 ACAAGCAAGGCGCTTCGCGGAACAGATCCAAATCAAAAGATTTTATACATCCATTTAC 480
 DB 421 ACAAGCAAGGCGCTTCGCGGAACAGATCCAAATCAAAAGATTTTATACATCCATTTAC 480
 OY 481 AGCAATGCCGATATGATGTCATGAATTAATTAAGAAATTAAGAGCGTCTAAAAACGTT 540
 DB 481 AGCAATGCCGATATGATGTCATGAATTAATTAAGAAATTAAGAGCGTCTAAAAACGTT 540
 OY 541 CAAATTCATGCGCTGGGACATTTGTTTATGATGAACAGCAAGTCAACGCTGAT 600
 DB 541 CAAATTCATGCGCTGGGACATTTGTTTATGATGAACAGCAAGTCAACGCTGAT 600
 OY 601 AAAGAGAGCTGACGCGGCGGCGCAAAATACGAATTA 639
 DB 601 AAAGAGAGCTGACGCGGCGGCGCTCAATACGAATTA 639

RESULT 6
 ABA96150
 ID ABA96150 standard; DNA: 639 BP.

XX ABA96150;

XX 16-APR-2002 (first entry)

XX *Bacillus circulans lipase 396 gene.*

XX Lipase 396: spore protein application; immune response; HIV; cancer;
 KW autoimmune disorder; inflammatory; allergic reaction; autoantigen;
 KW gene; ds.

XX *Bacillus circulans.*

XX key Location/Qualifiers

XX CDS 1..639

XX /tag=a

XX /product="lipase 396"

XX MO200200232-A2.

XX 03-JAN-2002.

XX 26-JUN-2001; 2001MO-US20372.

XX 26-JUN-2000; 2000US-214161P.

XX (MAXY-) MAXYGEN INC.

XX Goldman S, Lathrop SJ, Longchamp PF, Whalen RG;

XX WPI: 2002-147853/19.

XX Composition for modulating immune response, comprises a spore system
 XX having a spore and polypeptide, carbohydrate or nucleotide sequence
 XX having anti-pathogenic activity

XX Example 6: Page 136; 137pp; English.

XX The sequence represents the *Bacillus circulans lipase 396 gene*, which was
 XX inserted into the ColE sequence in the invention. The invention relates
 XX to novel compositions and methods for utilizing spore systems for
 XX medicinal and industrial protein applications. The peptides,
 XX polypeptides, proteins, and nucleic acids of interest in the invention
 XX may be useful for modulating an immune response. A spore system of the
 XX invention may function as a therapeutic, prophylactic, or immunology
 XX agent or vaccine against a disease or disease-inducing pathogen. A spore
 XX system may be designed to display a HIV antigen, or a disease-associated
 XX antigen such as cancer antigens, antigens associated with autoimmunity
 XX disorders, antigens associated with inflammatory conditions, antigens
 XX associated with allergic reactions, antigens associated with infectious
 XX agents, and autoantigens.

XX Sequence 639 BP; 201 A; 122 C; 157 G; 159 T; 0 other;

Query Match 98.0%; Score 626.2; DB 24; Length 639;
 Best Local Similarity 98.7%; Pred. No. 4.3e-186;
 Matches 631; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 ATGAATTTGTAAGAAAGATCATGCACTTGTACAAATTTGGTGTGACAGCACA 60
 DB 1 ATGAATTTTATAAGAAAGATCATGCACTTGTACAAATTTGGTGTGACAGCACA 60
 OY 61 TCGCTGTTTGCATGACGCGCTCAGCAAAAGCCGCTGAACACATTCAGTTGTATGTT 120
 DB 61 TCGCTGTTTGCATGACGCGCTCAGCAAAAGCCGCTGAACACATTCAGTTGTATGTT 120
 OY 121 CACGGTATCGAGAGCTTCATACAAATTTGGGGAATTAAGAGCTATCTCTATCTCAG 180
 DB 121 CACGGTATCGAGAGCTTCATACAAATTTGGGGAATTAAGAGCTATCTCTATCTCAG 180
 OY 181 GGCTGTACGGGGGAGAGCTGTATGCGTTTGGGACACAGGAGCGAATTT 240
 DB 181 GGCTGTACGGGGGAGAGCTGTATGCGTTTGGGACACAGGAGCGAATTT 240
 OY 241 AACCAATGCGCCGCTATTTACAGATTTTGCAAAAGGTTTGTAGAGCAAAAGCGGTGCGA 300
 DB 241 AACCAATGCGCCGCTATTTACAGATTTTGCAAAAGGTTTGTAGAGCAAAAGCGGTGCGA 300
 OY 301 AAAGTGAATTTGTGCTCAGATTTGGTGGCGGACACACCTTACTACATAAAAT 360
 DB 301 AAAGTGAATTTGTGCTCAGATTTGGTGGCGGACACACCTTACTACATAAAAT 360
 OY 361 CTGAGCGGCGGAAATTAATTAAGAAAGCTGTACGCTTGGGCGGCGAAGCGTTGCGAG 420

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|||||
Db 361 CTGACGCGCGAAATTAATGAACGCTGTAACGCTGGCGGCGGAACCGTTTGACG 420
OY 421 ACAAGCAAGGCGCTTCGGGGACAGATCCAAATCAAAAGATTTATACATTCATTAC 480
Db 421 ACAAGCAAGGCGCTTCGGGGACAGATCCAAATCAAAAGATTTATACATTCATTAC 480
OY 481 AGCAGTCCCGATATGATGTCATGAATTAATCAAAATTAAGACGGTGTAAAAAGCT 540
Db 481 AGCAGTCCCGATATGATGTCATGAATTAATCAAAATTAAGACGGTGTAAAAAGCT 540
OY 541 CAAATTCATGGCTTGGGACATTTGTTTATGATGAACAGCCAAATCAAGCTGATT 600
Db 541 CAAATTCATGGCTTGGGACATTTGTTTATGATGAACAGCCAAATCAAGCTGATT 600
OY 601 AAAGAGAGACTGAACGGCGGGGCCAAATATACGAATTA 639
Db 601 AAAGAGAGACTGAACGGCGGGGCCCTCAATACAAATTA 639

RESULT 7
ABK33824
ID ABK33824 standard; DNA: 639 BP.
AC ABR33824;
XX 08-MAY-2002 (first entry)
DE Bacillus lipase polynucleotide #6.
XX
XX Lipase; Bacillus; animal feed; flavour modification; fat modification;
XX human foodstuff; cheese; food emulsifier; leather tanning; gene; ds;
XX leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
XX coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
XX gastrointestinal lipid related condition; anti-inflammatory; respiratory;
XX gastrointestinal.
XX
XX Bacillus azotofornans.
XX
XX WO200206457-A2.
XX
XX 24-JAN-2002.
XX
XX 13-JUL-2001; 2001WO-US22160.
XX
XX 13-JUL-2000; 2000US-217954P.
XX
XX 21-JUN-2001; 2001US-300378P.
XX
XX (MAXY-) MAXYGEN INC.
XX
XX Giver LJ, Minshull J, Vogel K;
XX
XX WPI; 2002-171805/22.
XX
XX P-PSDB; AAU83846.
XX
XX Nucleic acids encoding lipase enzymes which are useful as supplements
XX in animal feeds, as agents of flavour modification and for treating
XX Crohn's disease and coeliac disease -
XX
XX Claim 81; Page 119; 196pp; English.
XX
XX The invention relates to new Bacillus lipase enzymes and the nucleic
XX acids encoding them. The lipase polypeptides are useful as supplements in
XX animal feeds, as agents of flavour modification and fat modification in
XX human foodstuffs (e.g. cheese), as agents in the creation of food
XX emulsifiers, as agents for tanning/processing of leather and as cleaning
XX agents. They are also useful for treating Crohn's disease, cystic
XX fibrosis, coeliac disease, indigestion, obesity and other
XX gastrointestinal mal-absorption problems. Gastrointestinal lipid related
XX conditions can be therapeutically or prophylactically treated via a
XX method of hydrolysing a lipid comprising expressing in a target cell or
XX contacting a target cell with an effective amount of DNA or protein of
XX the invention. Sequences ABK33819-ABK33874 represent Bacillus lipase

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CC polynucleotides of the invention.
XX
SQ Sequence 639 BP; 201 A; 121 C; 159 G; 158 T; 0 other;
Query Match 97.5%; Score 623; DB 24; Length 639;
Best Local Similarity 98.4%; Pred. No. 4,4e-185;
Matches 629; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
OY 1 -ATGAATTTGTAAGAAAGAGATCATTCACCTTTAACAATTTGGTGTGACAGTACA 60
Db 1 ATGAATTTGTAAGAAAGAGATCATTCACCTTTAACAATTTGGTGTGACAGTACA 60
OY 61 TCGCTGTTGGCATGACAGCCGTACGAAAAGCCGCTGACAAACATCCAGTTGATTGCTT 120
Db 61 TCGCTGTTGGCATGACAGCCGTACGAAAAGCCGCTGACAAACATCCAGTTGATTGCTT 120
OY 121 CACGCTATCGAGAGAGCTTCATACAAATTTGGCGGAAATTAAGACTATTCGTATCTCAG 180
Db 121 CACGCTATCGAGAGAGCTTCATACAAATTTGGCGGAAATTAAGACTATTCGTATCTCAG 180
OY 181 GCGTGTACAGCGGCGCAAGCTGATGCGTTGATTTTGGGCAAGACAGGAGCAATTAAT 240
Db 181 GCGTGTACAGCGGCGCAAGCTGATGCGTTGATTTTGGGCAAGACAGGAGCAATTAAT 240
OY 241 AACATGCGCCCGGATTAATACAGATTTGTGCAAAAAGCTTTAGACGAACGGGTGCGAAA 300
Db 241 AACATGCGCCCGGATTAATACAGATTTGTGCAAAAAGCTTTAGACGAACGGGTGCGAAA 300
OY 301 AAATGATATTTGCGTCACAGATGAGTGGGCGCGCAACACCTTACTCATTAATAAAT 360
Db 301 AAATGATATTTGCGTCACAGATGAGTGGGCGCGCAACACCTTACTCATTAATAAAT 360
OY 361 CTGAGACGGCGGAATTAATTAAGAAACGTGTAACGCTTGGCGGCGCAACCGTTGACAG 420
Db 361 CTGAGACGGCGGAATTAATTAAGAAACGTGTAACGCTTGGCGGCGCAACCGTTGACAG 420
OY 421 ACAAGCAAGGCGCTTCGGGGACAGATCCAAATCAAAAGATTTATACATTCATTAC 480
Db 421 ACAAGCAAGGCGCTTCGGGGACAGATCCAAATCAAAAGATTTATACATTCATTAC 480
OY 481 AGCAGTCCCGATATGATGTCATGAATTAATCAAAATTAAGACGGTGTAAAAAGCT 540
Db 481 AGCAGTCCCGATATGATGTCATGAATTAATCAAAATTAAGACGGTGTAAAAAGCT 540
OY 541 CAAATTCATGGCTTGGGACATTTGTTTATGATGAACAGCCAAATCAAGCTGATT 600
Db 541 CAAATTCATGGCTTGGGACATTTGTTTATGATGAACAGCCAAATCAAGCTGATT 600
OY 601 -AAAGAGAGACTGAACGGCGGGGCCAAATATACGAATTA 639
Db 601 -AAAGAGAGACTGAACGGCGGGGCCCTAGATACAAATTA 639

RESULT 8
ABK33821
ID ABK33821 standard; DNA: 639 BP.
AC ABR33821;
XX
XX 08-MAY-2002 (first entry)
XX
XX Bacillus lipase polynucleotide #3.
XX
XX Lipase; Bacillus; animal feed; flavour modification; fat modification;
XX human foodstuff; cheese; food emulsifier; leather tanning; gene; ds;
XX leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
XX coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
XX gastrointestinal lipid related condition; anti-inflammatory; respiratory;
XX gastrointestinal.
XX
XX Bacillus megaterium.
XX
XX WO200206457-A2.
XX
XX

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AC ABK33827;
XX 08-MAY-2002 (first entry)
XX
DE Bacillus lipase polynucleotide #9.
XX
KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; gene; ds;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
KW gastrointestinal.
XX
OS Bacillus sp.
XX
PN WO200206457-A2.
XX
PD 24-JAN-2002.
XX
PF 13-JUL-2001; 2001WO-US22160.
XX
PR 13-JUL-2000; 2000US-217954P.
XX
PR 21-JUN-2001; 2001US-300378P.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Giver LJ, Minshull J, Vogel K;
XX
XX WPI: 2002-171805/22.
DR P-PSDB: AAU83849.
XX
PT Nucleic acids encoding lipase enzymes which are useful as supplements
PT in animal feeds, as agents of flavour modification and for treating
PT Crohn's disease and coeliac disease -
XX
PS Claim 81; Page 120; 196pp; English.
XX
XX The invention relates to new Bacillus lipase enzymes and the nucleic
XX acids encoding them. The lipase polypeptides are useful as supplements in
XX animal feeds, as agents of flavour modification and fat modification in
XX human foodstuffs (e.g. cheese), as agents in the creation of food
XX emulsifiers, as agents for tanning/processing of leather and as cleaning
XX agents. They are also useful for treating Crohn's disease, cystic
XX fibrosis, coeliac disease, indigestion, obesity and other
XX gastrointestinal mal-absorption problems. Gastrointestinal lipid related
XX conditions can be therapeutically or prophylactically treated via a
XX method of hydrolysing a lipid comprising expressing in a target cell or
XX contacting a target cell with an effective amount of DNA or protein of
XX the invention. Sequences ABK33819-ABK33874 represent Bacillus lipase
XX polynucleotides of the invention.
XX
SQ Sequence 639 BP; 196 A; 127 C; 159 G; 157 T; 0 other;

Query Match 88.0%; Score 562.2; DB 24; Length 639;
Best Local Similarity 92.5%; Pred. No. 5.2e-166;
Matches 591; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 ATGAATTTTGTAAAAAGAGATCATTTGACATTTGTCCTGTCATCA 60
DB 1 ATGAATTTTGTAAAAAGAGATCATTTGACATTTGTCCTGTCATCA 60
QY 61 TCGCTGTTGGATGCACCCGTCAGCAAAAGCCGCTGACACATTCAGTTGATGCTT 120
DB 61 TCGCTGTTGGATGCACCCGTCAGCAAAAGCCGCTGACACATTCAGTTGATGCTT 120
QY 121 CACGGTATCGAGAGAGCTTCATACATTTTCCGGCAATTAAGAGCTATCTGATCTCAG 180
DB 121 CACGGTATCGAGAGAGCTTCATACATTTTCCGGCAATTAAGAGCTATCTGATCTCAG 180
QY 181 GGTGCTACAGCGGCAAGCTGATGCGGTGATTTTGGGCAAGACAGGAGCAATAT 240
DB 181 GGTGCTACAGCGGCAAGCTGATGCGGTGATTTTGGGCAAGACAGGAGCAATAT 240

QY 241 AACAAATGCCCCGGTATATATACAGATTTTGCAAAAGGTTTAGACGAAAGCGGTCGAAA 300
DB 241 AACAAATGCCCCGGTATATATACAGATTTTGCAAAAGGTTTAGACGAAAGCGGTCGAAA 300
QY 301 AAAGTGATATTTGCTGCCTACAGTATGGTGGCGGCAACACACCTTACTACTATAAAAAAT 360
DB 301 AAAGTGATATTTGCTGCCTACAGTATGGTGGCGGCAACACACCTTACTACTATAAAAAAT 360
QY 361 CCGGACGGCGGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
DB 361 CCGGACGGCGGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
QY 421 ACAGCAAGGCGCTTCGCGGACAGATCCAAATTCAAAGATTTTATACATTCATTTAC 480
DB 421 ACAGCAAGGCGCTTCGCGGACAGATCCAAATTCAAAGATTTTATACATTCATTTAC 480
QY 481 AGCAGTCCCGATATATATGTCATGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 540
DB 481 AGCAGTCCCGATATATGTCATGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 540
QY 541 CAAATTCATGCGCTGGCGACATGTTGATGATGACAGCAGCAGCAGCAGCAGCAGCAGCAGT 600
DB 541 CAAATTCATGCGCTGGCGACATGTTGATGATGACAGCAGCAGCAGCAGCAGCAGCAGCAGT 600
QY 601 AAGAGAGAGCTGAGAGCGGCGGCGCCAAATACGAATTA 639
DB 601 AAGAGAGAGCTGAGAGCGGCGGCGCCCAATACGAATTA 639

RESULT 12
ABK33842
ID ABK33842 standard; DNA; 544 BP.

ABK33842;

08-MAY-2002 (first entry)

Bacillus lipase polynucleotide #24.

Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; gene; ds;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
KW gastrointestinal.

Synthetic.

WO200206457-A2.

24-JAN-2002.

13-JUL-2001; 2001WO-US22160.

13-JUL-2000; 2000US-217954P.

21-JUN-2001; 2001US-300378P.

(MAXY-) MAXYGEN INC.

Giver LJ, Minshull J, Vogel K;

WPI: 2002-171805/22.

P-PSDB: AAU83864.

Nucleic acids encoding lipase enzymes which are useful as supplements
PT in animal feeds, as agents of flavour modification and for treating
PT Crohn's disease and coeliac disease -

Claim 81; Page 127; 196pp; English.

The invention relates to new Bacillus lipase enzymes and the nucleic
XX acids encoding them. The lipase polypeptides are useful as supplements in
XX animal feeds, as agents of flavour modification and fat modification in

CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences ABK3819-ABK3874 represent *Bacillus* lipase
CC polynucleotides of the invention.

XX
SQ Sequence 544 BP: 170 A; 103 C; 141 G; 130 T; 0 other:

Query Match 81.9%; Score 523.2; DB 24; Length 544;
Best Local Similarity 97.6%; Pred. No. 8.2e-154;

Matches 531; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

```
OY 96 TGAACACATCCAGTTGTTATGTTTCACGGATGCGAGGACCTTCATCATTTTGGCGG 155
   |||||||
DB 1 TGAACACATCCAGTTGTTATGTTTCACGGATGCGAGGACCTTCATCATTTTGGCGG 60
OY 156 AATTAGAGCTATCTCGATCTCAGGGCTGCTCAGCGGGCAAGCTGTATGCGGTTGATT 215
   |||||||
DB 61 AATTAGAGCTATCTCGATCTCAGGGCTGCTCAGCGGGCAAGCTGTATGCGGTTGATT 120
OY 216 TTGGGACACAGCAGGAGCAATTTAACAATGCCCGGTTATTCACGATTTCGCCAANA 275
   |||||||
DB 121 TTGGGACACAGCAGGAGCAATTTAACAATGCCCGGTTATTCACGATTTCGCCAANA 180
OY 276 GGTTTAGACGAACGGGTGCGAANAAGTGATATTCCTCCTACAGATATGGGTCGCGC 335
   |||||||
DB 181 GGTTTAGACGAACGGGTGCGAANAAGTGATATTCCTCCTACAGATATGGGTCGCGC 240
OY 336 GAACACACCTTACTACATATAAAAACTGACGGCGGAATTAATGAAAACTGCTAAC 395
   |||||||
DB 241 GAACACACCTTACTACATATAAAAACTGACGGCGGAATTAATGAAAACTGCTAAC 300
OY 396 GCTTGGGGCGCGCAACGCTTGACGACGAAGAAGCGCTTCGCGGACAGATCCAAATCA 455
   |||||||
DB 301 GCTTGGGGCGCGCAACGCTTGACGACGAAGAAGCGCTTCGCGGACAGATCCAAATCA 360
OY 456 AAGATTTTATACATCATTTTACAGACGATGCGGATATGATTCATGATTTACTTATC 515
   |||||||
DB 361 AAGATTTTATACATCATTTTACAGACGATGCGGATATGATTCATGATTTACTTATC 420
OY 516 AAAATTAGAGCGGTCTAAAAAGCTCAAAATTCATGCGCTGGGACATTTGTTATTGAT 575
   |||||||
DB 421 AAAATTAGAGCGGTCTAAAAAGCTCAAAATTCATGCGCTGGGACATTTGTTATTGAT 480
OY 576 GAACAGCAATTCACAGCCTTGATTAAGAAGACTGAACGGCGGGGCCAAATATAGCAA 635
   |||||||
DB 481 GAACAGCAATTCACAGCCTTGATTAAGAAGACTGAACGGCGGGGCCAAATATAGCAA 540
OY 636 TTAA 639
   || |
DB 541 TTGA 544
```

RESULT 13

ABK3871 ID ABK3871 standard; DNA; 544 BP.

XX

AC ABK3871:

DT 08-MAY-2002 (first entry)

XX

DE *Bacillus* lipase polynucleotide #53.

XX

Lipase; *Bacillus*; animal feed; flavour modification; fat modification;

human foodstuff; cheese; food emulsifier; leather tanning; gene; ds;

leather processing; cleaning agent; Crohn's disease; cystic fibrosis;

coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;

gastrointestinal lipid related condition; anti-inflammatory; respiratory;

KW gastrointestinal.

XX Synthetic.

OS W0200206457-A2.

PN 24-JAN-2002.

PD 13-JUL-2001; 2001WO-US22160.

PF 13-JUL-2000; 2000US-217954P.

PR 21-JUN-2001; 2001US-300378P.

XX (MAXY-) MAXYGEN INC.

XX Glycer LJ, Minshall J, Vogel K;

XX WPI: 2002-171805/22.

DR P-PSDB; AA083893.

XX Nucleic acids encoding lipase enzymes which are useful as supplements

PT in animal feeds, as agents of flavour modification and for treating

PT Crohn's disease and coeliac disease.

XX Claim 81; Page 137-138; 196pp; English.

XX The invention relates to new *Bacillus* lipase enzymes and the nucleic

CC acids encoding them. The lipase polypeptides are useful as supplements in

CC animal feeds, as agents of flavour modification and fat modification in

CC human foodstuffs (e.g. cheese), as agents in the creation of food

CC emulsifiers, as agents for tanning/processing of leather and as cleaning

CC agents. They are also useful for treating Crohn's disease, cystic

CC fibrosis, coeliac disease, indigestion, obesity and other

CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related

CC conditions can be therapeutically or prophylactically treated via a

CC method of hydrolysing a lipid comprising expressing in a target cell or

CC contacting a target cell with an effective amount of DNA or protein of

CC the invention. Sequences ABK3819-ABK3874 represent *Bacillus* lipase

CC polynucleotides of the invention.

XX

SQ Sequence 544 BP: 172 A; 102 C; 138 G; 132 T; 0 other:

Query Match 81.9%; Score 523.2; DB 24; Length 544;

Best Local Similarity 97.6%; Pred. No. 8.2e-154;

Matches 531; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

```
OY 96 TGAACACATCCAGTTGTTATGTTTCACGGATGCGAGGACCTTCATCATTTTGGCGG 155
   |||||||
DB 1 TGAACACATCCAGTTGTTATGTTTCACGGATGCGAGGACCTTCATCATTTTGGCGG 60
OY 156 AATTAGAGCTATCTCGATCTCAGGGCTGCTCAGCGGGCAAGCTGTATGCGGTTGATT 215
   |||||||
DB 61 AATTAGAGCTATCTCGATCTCAGGGCTGCTCAGCGGGCAAGCTGTATGCGGTTGATT 120
OY 216 TTGGGACACAGCAGGAGCAATTTAACAATGCCCGGTTATTCACGATTTCGCCAANA 275
   |||||||
DB 121 TTGGGACACAGCAGGAGCAATTTAACAATGCCCGGTTATTCACGATTTCGCCAANA 180
OY 276 GGTTTAGACGAACGGGTGCGAANAAGTGATATTCCTCCTCACAAGATATGGTGGCGC 335
   |||||||
DB 181 GGTTTAGACGAACGGGTGCGAANAAGTGATATTCCTCCTCACAAGATATGGTGGCGC 240
OY 336 GAACACACCTTACTACATATAAAAACTGACGGCGGAATTAATGAAAACTGCTAAC 395
   |||||||
DB 241 GAACACACCTTACTACATATAAAAACTGACGGCGGAATTAATGAAAACTGCTAAC 300
OY 396 GCTTGGGGCGCGCAACGCTTGACGACGAAGAAGCGCTTCGCGGACAGATCCAAATCA 455
   |||||||
DB 301 ACTTGGGGCGCGCAATGCTTGACGACGAAGAAGCGCTTCGCGGACAGATCCAAATCA 360
OY 456 AAGATTTTATACATCATTTTACAGACGATGCGGATATGATTCATGATTTACTTATC 515
   |||||||
DB 361 AAGATTTTATACATCATTTTACAGACGATGCGGATATGATTCATGATTTACTTATC 420
```


Job time : 160 secs

PI Giver LJ, Minshall J, Vogel K;
XX
XX WPI; 2002-171805/22.
DR P-PSDB; AA083883.
XX

PT Nucleic acids encoding lipase enzymes which are useful as supplements
PT in animal feeds, as agents of flavour modification and for treating
PT Crohn's disease and coeliac disease -
XX
XX

PS Claim 81, Page 134, 196pp: English.

CC The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences ABK3819-ABK3874 represent Bacillus lipase
CC polynucleotides of the invention.
XX
XX

SQ Sequence 544 BP: 170 A; 104 C; 140 G; 130 T; 0 other;

Query Match 81.6%; Score 521.6; DB 24; Length 544;
Best Local Similarity 97.4%; Pred. No. 2.6e-153;

Matches 530; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 96 TGAACACATTCAGTCTGTATGTTACAGGTATCGAGAGAGCTTCATACATTTTGGCGG 155
DB 1 TGAACACATTCAGTCTGTATGTTACAGGTATCGAGAGAGCTTCATACATTTTGGCGG 60
QY 156 AATTAAGAGCTATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 215
DB 61 AATTAAGAGCTATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 120
QY 216 TTGGGACAAAGCAGGAGGATTTAACAATGCCGATATTATCAGATTTGTGCAAAA 275
DB 121 TTGGGACAAAGCAGGAGGATTTAACAATGCCGATATTATCAGATTTGTGCAAAA 180
QY 276 GCTTTAGAGAAACGGGTGCAAAAAGTGATATTGCTCTCAGATATGGGTGGCGC 335
DB 181 GCTTTAGAGAAACGGGTGCAAAAAGTGATATTGCTCTCAGATATGGGTGGCGC 240
QY 336 GAACACACCTTACTACATTAATAATCTGACGGCGGAAATTAATTAATAATTAATAATTAATA 395
DB 241 GAACACACCTTACTACATTAATAATCTGACGGCGGAAATTAATTAATAATTAATAATTAATA 300
QY 396 GCTTTGGGCGGCGGAGCGGCTGACAGCAAGGCGCTTCGGGAAACAGATCCAAATCA 455
DB 301 GCTTTGGGCGGCGGAGCGGCTTGGACAGCAAGGCGCTTCGGGAAACAGATCCAAATCA 360
QY 456 AAGATTTTATACATTCATTTACAGAGGCGGATATGATGTCATGATTTACTATATC 515
DB 361 AAGATTTTATACATTCATTTACAGAGGCGGATATGATGTCATGATTTACTATATC 420
QY 516 AATTAAGAGCTATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 575
DB 421 AATTAAGAGCTATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 480
QY 576 GAACAGCAAGCTCAACAGCTGATTTAAGAAGAGACTGAACGGCGGGGCCAAATACGAA 635
DB 481 GAACAGCAAGCTCAACAGCTGATTTAAGAAGAGACTGAACGGCGGGGCCAAATACGAA 540
QY 636 TTAA 639
DB 541 TTGA 544

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2003, 06:05:53 ; Search time 43 Seconds
(without alignments)
4557.359 Million cell updates/sec

Title: US-09-905-666A-1

Perfect score: 639

Sequence: 1 atgaatttgtaaaagaag.....ggggccaataacgaattaa 639

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA: *
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/Backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Match	Length	ID	Description
No.	Score	Match	Length	ID	Description
1	297.6	46.6	793	1 US-07-930-678-1	Sequence 1, Appli
2	42.2	6.6	7218	1 US-08-232-463-14	Sequence 14, Appl
3	36.2	5.7	502	4 US-09-280-116-70	Sequence 70, Appl
4	33.2	5.2	1089	3 US-08-978-589A-1	Sequence 1, Appli
5	33.2	5.2	1089	4 US-09-336-601-2	Sequence 2, Appli
6	32.2	5.0	1194	4 US-09-466-257A-7	Sequence 7, Appli
7	32.2	5.0	1194	4 US-09-466-257A-9	Sequence 9, Appli
8	32.2	5.0	1424	1 US-08-723-886-2	Sequence 2, Appli
9	32.2	5.0	1424	4 US-08-424-797A-2	Sequence 9, Appli
10	31.8	5.0	954	4 US-09-134-001C-529	Sequence 529, App
11	31.8	4.9	99500	4 US-09-798-096-10	Sequence 10, Appl
12	30.8	4.8	1684	4 US-08-961-527-258	Sequence 258, App
13	30.8	4.8	6030	1 US-08-441-139-8	Sequence 8, Appli
14	30.4	4.8	289	4 US-09-007-005-17	Sequence 17, Appl
15	30.4	4.8	289	4 US-09-244-796-17	Sequence 17, Appl
16	30.4	4.8	289	4 US-09-227-357-149	Sequence 149, App
17	30.4	4.7	1194	4 US-09-134-001C-2256	Sequence 2256, Ap
18	29.8	4.7	307	4 US-09-198-083-4	Sequence 4, Appli
19	29.8	4.7	307	4 US-09-862-167-4	Sequence 4, Appli
20	29.8	4.7	3918	3 US-08-836-329-1	Sequence 1, Appli
21	29.8	4.7	5757	4 US-08-984-618-1	Sequence 1, Appli
22	29.6	4.6	6765	2 US-08-677-010-2	Sequence 2, Appli
23	29.6	4.6	6765	2 US-08-790-519-2	Sequence 1, Appli
24	29.6	4.6	9581	2 US-08-677-010-1	Sequence 1, Appli
25	29.6	4.6	9581	2 US-08-790-519-1	Sequence 8, Appli
26	29.4	4.6	816	3 US-08-968-563-8	Sequence 8, Appli
27	29.4	4.6	816	3 US-08-969-683A-8	Sequence 8, Appli

28	29.4	4.6	816	4 US-09-297-928-4	Sequence 4, Appli
29	29.2	4.6	1330	2 US-09-036-582-33	Sequence 33, Appl
30	29.2	4.6	2118	1 US-08-400-422-5	Sequence 5, Appli
31	29.2	4.6	3872	2 US-08-331-081B-4	Sequence 4, Appli
32	29	4.5	1099	4 US-09-072-596-320	Sequence 320, App
33	29	4.5	1716	3 US-08-656-034-9	Sequence 9, Appli
34	29	4.5	2160	3 US-08-656-034-1	Sequence 1, Appli
35	28.6	4.5	711	4 US-09-134-001C-1248	Sequence 1248, Ap
36	28.6	4.5	1524	1 US-08-409-132-1	Sequence 1, Appli
37	28.6	4.5	1524	2 US-08-408-669-1	Sequence 1, Appli
38	28.6	4.5	1720	4 US-08-235-836C-111	Sequence 111, App
39	28.6	4.5	2102	4 US-08-235-836C-65	Sequence 65, Appl
40	28.6	4.5	2107	4 US-08-235-836C-73	Sequence 73, Appl
41	28.6	4.5	2258	1 US-07-720-589-1	Sequence 1, Appli
42	28.6	4.5	2258	2 US-08-785-190-1	Sequence 1, Appli
43	28.6	4.5	2258	5 PCT-US92-05539-1	Sequence 1, Appli
44	28.4	4.4	2900	1 US-08-034-650-9	Sequence 9, Appli
45	28.4	4.4	2900	1 US-08-449-015-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-07-930-678-1
Sequence 1, Application US/07930678
Patent No. 5427936
GENERAL INFORMATION:
APPLICANT: MOELLER, Bernhard
APPLICANT: VETTER, Roman
APPLICANT: WILKE, Detlef
APPLICANT: FOULLOIS, Birgit
TITLE OF INVENTION: Alkaline Bacillus Lipases, Coding DNA
TITLE OF INVENTION: Sequences Therefor and Bacilli, Which Produce These
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/930, 678
FILING DATE: 19921013
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP91/00664
FILING DATE: 08-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 40 12 070.8
FILING DATE: 14-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, J.D.
REGISTRATION NUMBER: 26, 269
REFERENCE/DOCKET NUMBER: 16877/318/KACH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)836-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

RESULT 4
 US-08-978-589A-1
 Sequence 1, Application US/08978589A
 Patent No. 6087145
 GENERAL INFORMATION:
 APPLICANT: ISHII, Takeshi
 APPLICANT: MITSUO, Satoshi
 TITLE OF INVENTION: ESTERASE GENE AND ITS USE
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
 STREET: P.O. BOX 747
 CITY: FALLS CHURCH
 STATE: VIRGINIA
 COUNTRY: UNITED STATES OF AMERICA
 ZIP: 22040
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/978,589A
 FILING DATE: 26-NOV-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Murphy Jr, Gerald M.
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 20-4336P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 205-8000
 TELEFAX: (703) 205-8050
 INFORMATION FOR SEQ ID NO: 1:

US-09-466-257A-7
 RESULT 6
 : Sequence 7, Application US/09466257A-7
 : Patent No. 6337190
 : GENERAL INFORMATION:
 : APPLICANT: Hwang, Tzann-Shun
 : APPLICANT: Wu, Szu-Pei
 : APPLICANT: Chou, Hsin-Hua
 : APPLICANT: Yen, Hwa-Yi
 : APPLICANT: Lin, Lung-Shen


```

CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,797A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: 27127/32582
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1424 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 427..1278
US-08-424-797A-2

Query Match
Best Local Similarity 5.0%; Score 32.2; DB 4; Length 1424;
Matches 67; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 425 GCAAGCGCTTCGGGACACGATCAATCAAAAGATTTTATACATCCATTACAGCA 484
DB 881 GCGCGGTACTTGGAAACAGAGCATCTGAAAGAGTTGTTACGAAGCCATTTCACCC 940
QY 485 GTCCGATATGATGTGATGATTAATCAAAATTAAGCGGTGCTAAACGCTCAAA 544
DB 941 GTGAGATATTTATCACAAGATGTTCTTCGCTAATGCTATGATTAAGATGTAAC 1000
QY 545 TTGAT 549
DB 1001 TTTAT 1005

RESULT 10
US-09-134-001C-529/c
Sequence 529, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 529
LENGTH: 954
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-529
```

```

Query Match
Best Local Similarity 5.0%; Score 31.8; DB 4; Length 954;
Matches 51; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 455 AAAAGATTTTATACATCATTTTACAGCAGTCCGATATGATGTCATGATTAAT 514
DB 920 ACAAGATTTTGTACAAATATTTTACAGTGTGATGATGATGATGATGATTTTA 861
QY 515 CAAATTTAGACGGTGTCAAAAC 537
DB 860 CTAAGTCTCATTAATATATC 838

RESULT 11
US-09-798-096-10
Sequence 10, Application US/0798096
Patent No. 6399378
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
TITLE OF INVENTION: ANTISENSE MODULATION OF RECOL2 EXPRESSION
FILE REFERENCE: RTS-0207
CURRENT APPLICATION NUMBER: US/09/798,096
CURRENT FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 10
LENGTH: 99500
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-798-096-10

Query Match
Best Local Similarity 4.9%; Score 31; DB 4; Length 99500;
Matches 103; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 226 ACAGGCGCATTTAATCAATGCGCCGTTATATACAGATTTTGCAGAAAGTTTAGAC 285
DB 21734 ACAAGGGACATTTATATCATGATTTACAGAGTAAAGATTTATAGAGATTTGGAG 21793
QY 286 GAAAGGGGTGCGAAAGAGTGAATTTGCTGACAGTATGGGTGGCGGAACACCT 345
DB 21794 CAATGATGCGCAACAATTTGATTAATGAATGAATGAATGAATTCCTCAAAACACAT 21853
QY 346 TACTACATTAATAATCTGAGCGCGGAAATTAATTAACGTCATACGCTTGGCGGC 405
DB 21854 AACCCACAGACAGAAATCATGAAGAAACAGAAATCTGAACACACCTATTAAGTAAGG 21913
QY 406 GCGAAGCGTTGACAGACAGCAAGCGCTTCCGGAACAGATC 448
DB 21914 AGATTGAGTTAGTATATCAGGTATCCACCAACAAAGAAAGCTC 21956

RESULT 12
US-08-961-527-258
Sequence 258, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESS: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
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SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 258:
SEQUENCE CHARACTERISTICS:
LENGTH: 1684 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-258

Query Match
Best Local Similarity 4.8%; Score 30.8; DB 4; Length 1684;
Matches 83; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 370 GGAATTAATTAAGAAACGCTGTAACGCTTGCGGCGGACCGCTTGCAGCAAGCAAG 429
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1371 GGAACGAGTTTGAACAGATAGATAGGTTGTTCCGAAATCCAGATACCTTACTT 1430
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 430 GCGCTCCGGGACAGATCCAAATCAAAAGATTTATACACATTCATTACAGCAGTGC 489
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1431 GCGTTTGTGACCTAGGTTGCTAAATGAACCTTAAATGAGTGCATTTCACTGAT 1490
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 490 GATATGATGTCATGATTAATTAATCAAAATTAAGACGGTCTAAACAGCC 539
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1491 AAAGTATCATCATCAACAGAGGTTCCAAATTGTAGAGAGTGCTATTAATGTC 1540
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
US-08-441-139-8
Sequence 8, Application US/08441139
Patent No. 5773245
GENERAL INFORMATION:
APPLICANT: Wiltup, Dr. Karl D.
APPLICANT: Robinson, Anne S.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESS: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: NY
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,139
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Digilio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8646
```

```
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 6030 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1004..4753
US-08-441-139-8

Query Match
Best Local Similarity 4.8%; Score 30.8; DB 1; Length 6030;
Matches 71; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 455 AAAGATTATACATCATTTACAGCAGTCCGATATGATTCATGATTAATTTAT 514
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 5452 AAAGTTTCTGAATTAACAAATTAACAGCTTATATCCAGCTGATTAATCCCACTAA 5511
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 515 CAAATTTAGACGCTCTATAAACGCTCAATTCATGCGCTTGCGCACATTTGTTATTGA 574
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 5512 CTAGAAAAGAAAGTTGTCAAACGCAATTAACAGAGATTGATTTTCAATCTTTAAACA 5571
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 575 TGACAGCAGCAAGTCAACA 592
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 5572 TCACACGCGACACACAAA 5589
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
US-09-007-005-17
Sequence 17, Application US/09007005B
Patent No. 6258558
GENERAL INFORMATION:
APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihue
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
FILE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Translation template
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(289)
OTHER INFORMATION: n = A,T,C or G
US-09-007-005-17

Query Match
Best Local Similarity 4.8%; Score 30.4; DB 4; Length 289;
Matches 5; Conservative 85; Mismatches 99; Indels 0; Gaps 0;

QY 264 ATTGTGCAAAAGGTTTAGACGAACGCGTCCGAAAGATGATATTTGCTGCTACAG 323
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27 RURURARCARARURURARARURGRNRNRNRNRNRNRNRNRNRNRNRNRNRNR 86
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 324 TATGTGCGCGGACACACACTTACTACATAAAAAATCTGGAGCGCGGAATAATTTGA 383
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 87 RNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRS 146
QY 384 AAACGTCGTAACGCTTGGGGCGGACCGCTCGAGACAGACAGCCCTCCGGGAC 443
Db 147 RNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRS 206
QY 444 AGATCCAAA 452
Db 207 RNRNRSRNR 215

RESULT 15

US-09-244-796-17
; Sequence 17, Application US/09244796
; Patent No. 6281344
; GENERAL INFORMATION:
; APPLICANT: Szoctak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihue
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350007
; CURRENT APPLICATION NUMBER: US/09/244,796
; EARLIER FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 09/007,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 289
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17

Query Match 4.8%; Score 30.4; DB 4; Length 289;
Best Local Similarity 2.6%; Pred.No.1.5;
Matches 5; Conservative 85; Mismatches 99; Indels 0; Gaps 0;

QY 264 ATTTGTCAAAAGTTTACGACGAGGCGGAAAAAGTGATATTGCTGCACAG 323
Db 27 RURURARARARARURARARARURGRNRSRNRNRSRNRNRSRNRNRS 86
QY 324 TATGGTGGCGGACACCTTACTACATAAAATCTGACGCGGAAATAAATGA 383
Db 87 RNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRS 146
QY 384 AAACGTCGTAACGCTTGGGGCGGACCGCTCGAGACAGACAGCCCTCCGGGAC 443
Db 147 RNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRS 206
QY 444 AGATCCAAA 452
Db 207 RNRNRSRNR 215

Search completed: May 18, 2003, 07:51:45
Job time : 92 secs

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GenCore version 5.1.4.P5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2003, 07:31:38 ; Search time 93 Seconds
(without alignments)
8863.124 Million cell updates/sec

Title: US-09-905-666a-1
Perfect score: 639
Sequence: 1 atgaattgttaaaagaag.....ggggccaaatacgaattaa 639

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 810007 seqs, 644969091 residues

Total number of hits satisfying chosen parameters: 1620014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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6: /cgn2-6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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13: /cgn2-6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
14: /cgn2-6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	626.2	98.0	639	12 US-10-028-247-3	Sequence 3, Appl1
2	38.2	6.0	1011	9 US-09-878-781-9	Sequence 17, Appl1
3	38.2	6.0	1011	10 US-09-878-766a-17	Sequence 1, Appl1
4	37.4	5.9	400	7 US-08-781-986a-4008	Sequence 4, Appl1
5	37.4	5.9	13321	7 US-08-781-986a-4	Sequence 855, App
6	35.8	5.6	785	9 US-09-991-936-852	Sequence 3605, App
7	34.6	5.4	545	9 US-09-938-842a-3605	Sequence 128, App
8	34.4	5.4	32768	10 US-09-070-927a-128	Sequence 412, App
9	33.8	5.3	545	9 US-10-184-644-412	Sequence 412, App
10	33.8	5.3	597	10 US-09-917-800a-846	Sequence 846, App
11	33.2	5.2	1089	9 US-10-147-467-1	Sequence 1, Appl1
12	33.2	5.2	1089	9 US-09-939-964-1	Sequence 18, Appl1
13	32.8	5.1	1884	10 US-09-731-872-18	Sequence 1896, App
14	32.6	5.0	432	10 US-09-974-300-1896	Sequence 667, App
15	32.2	4.9	382	10 US-09-880-107-667	Sequence 195, App
16	31.2	4.9	1180	10 US-09-881-752a-195	Sequence 60, Appl1
17	31.2	4.9	694	9 US-10-184-644-60	Sequence 60, Appl1
18	31	4.9	694	9 US-10-184-634-60	Sequence 60, Appl1
19	31	4.9	694	9 US-10-184-634-60	Sequence 60, Appl1

20	30.8	4.8	737	10 US-09-770-149-76	Sequence 76, Appl1
21	30.8	4.8	1011	9 US-09-878-781-11	Sequence 11, Appl1
22	30.8	4.8	1011	10 US-09-878-766a-19	Sequence 19, Appl1
23	30.8	4.8	2000	9 US-09-938-842a-3864	Sequence 3864, App
24	30.6	4.8	402	9 US-09-918-995-36871	Sequence 36871, A
25	30.6	4.8	1101	10 US-09-770-445-100	Sequence 100, App
26	30.6	4.8	1404	10 US-09-912-020-221	Sequence 221, App
27	30.6	4.8	1939	9 US-09-954-531-382	Sequence 382, App
28	30.2	4.7	433	10 US-09-867-901-1711	Sequence 1711, App
29	30.2	4.7	500	9 US-09-991-936-1676	Sequence 1676, App
30	30.2	4.7	594	9 US-10-123-155-10	Sequence 10, Appl1
31	30.2	4.7	2673	9 US-10-092-154-1876	Sequence 1876, App
32	30.2	4.7	2673	10 US-09-764-847-1876	Sequence 1876, App
33	30.2	4.7	249487	9 US-10-026-188-3	Sequence 3, Appl1
34	30.2	4.7	545	9 US-09-983-802-149	Sequence 149, App
35	30	4.7	83450	9 US-09-811-469-3	Sequence 3, Appl1
36	29.8	4.7	307	9 US-10-105-877-4	Sequence 4, Appl1
37	29.8	4.7	320	10 US-09-783-590-8898	Sequence 8898, App
38	29.8	4.7	400	7 US-08-781-986a-3578	Sequence 3578, App
39	29.8	4.7	545	10 US-09-864-761-8107	Sequence 8107, App
40	29.8	4.7	12658	7 US-08-781-986a-127	Sequence 127, App
41	29.6	4.6	1184	9 US-10-123-155-412	Sequence 412, App
42	29.6	4.6	5598	9 US-09-938-842a-1436	Sequence 1436, App
43	29.6	4.6	15856	9 US-09-764-891-8240	Sequence 8240, App
44	29.6	4.6	1691139	9 US-10-067-514-1	Sequence 1, Appl1
45	29.4	4.6	549	9 US-09-991-936-476	Sequence 476, App

ALIGNMENTS

RESULT 1
US-10-028-247-3
Sequence 3, Application US/10028247
Patent No. US20020150594A1
GENERAL INFORMATION:
APPLICANT: Goldman, Stanley
APPLICANT: Lathrop, Stephanie J.
APPLICANT: Longchamp, Pascal F.
APPLICANT: Whalen, Robert G.
APPLICANT: Maxygen, Inc.
TITLE OF INVENTION: Methods and Compositions for Developing Score Display
TITLE OF INVENTION: Systems for Medicinal and Industrial Applications
FILE REFERENCE: 18097a-03352005
CURRENT APPLICATION NUMBER: US/10/028,247
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US-60/214,164
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 09/892,208
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 639
TYPE: DNA
ORGANISM: Bacillus circulans
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(639)
OTHER INFORMATION: Lipase 396
US-10-028-247-3

Query Match 98.0% Score 626.2; DB 12; Length 639;
Best Local Similarity 98.7%; Pred No. 9.3e-187;
Matches 631; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 ATGAATTGTTGAAAAAGATCAATGACCTGTGATCAATTTGCTGCTACATCA 60
DB 1 ATGAATTATTAATAAAGATCAATGACCTGTGATCAATTTGCTGCTACATCA 60
QY 61 TCGCTGTTGCGATGACGCGCTGACGAAAGCGCTGAAACATTCAGTTTATGCTT 120
DB 61 TCGCTGTTGCGATGACGCGCTGACGAAAGCGCTGAAACATTCAGTTTATGCTT 120

QY 121 CACGATATCGAGAGAGCTTCATACATTTTCGGGAATTAAGACTATCTGTAATCTCAG 180
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Db 121 CACGATATCGAGAGAGCTTCATACATTTTCGGGAATTAAGACTATCTGTAATCTCAG 180
QY 181 GCGTGTGTCACGGGCGAGCTGTATGCGGTGATTTTGGGCAAGACAGGAGCAATAT 240
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Db 181 GCGTGTGTCACGGGCGAGCTGTATGCGGTGATTTTGGGCAAGACAGGAGCAATAT 240
QY 241 AACATATGCGCGGTATTTATCATCATTTGTGCAAAAGTTTATAGCAAGAGGTCGCAAA 300
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Db 241 AACATATGCGCGGTATTTATCATCATTTGTGCAAAAGTTTATAGCAAGAGGTCGCAAA 300
QY 301 AAATGATATTTGCTGCTACAGATATGGTGCGCGAAGACACCTTACTACATATAAAAT 360
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Db 301 AAATGATATTTGCTGCTACAGATATGGTGCGCGAAGACACCTTACTACATATAAAAT 360
QY 361 CTGACGCGCGGAATTAATTAAGTCTGTAACGCTGGCGCGGCAAGCCTTCGACG 420
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Db 361 CTGACGCGCGGAATTAATTAAGTCTGTAACGCTGGCGCGGCAAGCCTTCGACG 420
QY 421 ACAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAGATTTTATACATCATTTAC 480
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QY 481 AGCAGTCCCATATGATTTGATGATTAATTAATTAAGACGCTGCTAAAGCCT 540
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QY 541 CAAATTCATGCGCTTGGGACATGCTTTATTTGATGAACAGCCAGCTGAT 600
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Db 541 CAAATTCATGCGCTTGGGACATGCTTTATTTGATGAACAGCCAGCTGAT 600
QY 601 AAAGAGGACTGAACGCGGCGGCAAAATGAGATTA 639
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Db 601 AAAGAGGACTGAACGCGGCGGCTCAATACAAATTA 639

RESULT 2
US-09-878-781-9
; Sequence 9, Application US/09878781
; Publication No. US20030082781A1
; GENERAL INFORMATION:
; APPLICANT: Bolton, Alexandra J.
; APPLICANT: Perez-Casal, Jose
; APPLICANT: Fontaine, Michael
; APPLICANT: Potter, Andrew A.
; TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GAPC PROTEIN AGAINST
; FILE REFERENCE: 9000-0055
; CURRENT APPLICATION NUMBER: US/09/878,781
; CURRENT FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1011
; TYPE: DNA
; ORGANISM: Streptococcus parauberis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1011)
US-09-878-781-9

Query Match 6.08; Score 38.2; DB 9; Length 1011;
Best Local Similarity 56.98; Pred. No. 0.13;
Matches 70; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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Db 315 TGTCCAAAGGTTTATAGCAAGAGGTCGCAAAAGTGTATTTGCTGCTGCGTGG 374
QY 327 GCGTGGCGGCAACACCTTACTACATTAATAATCTGACGCGGCAATTAATTAATTA 386
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Db 327 GCGTGGCGGCAACACCTTACTACATTAATAATCTGACGCGGCAATTAATTAATTA 386

Db 375 AGATGACGTGAACACAGTTGATTTTAACTAACCAATGATATCTTATGAGACTGAAC 434
QY 387 CGT 389
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Db 435 AGT 437

RESULT 3
US-09-878-766A-17
; Sequence 17, Application US/09878766A
; Patent No. US20020044928A1
; GENERAL INFORMATION:
; APPLICANT: Potter, Andrew A.
; APPLICANT: Perez-Casal, Jose
; APPLICANT: Fontaine, Michael
; TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
; FILE REFERENCE: 9000-0057
; CURRENT APPLICATION NUMBER: US/09/878,766A
; CURRENT FILING DATE: 2001-09-10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 1011
; TYPE: DNA
; ORGANISM: Streptococcus parauberis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1011)
US-09-878-766A-17

Query Match 6.08; Score 38.2; DB 10; Length 1011;
Best Local Similarity 56.98; Pred. No. 0.13;
Matches 70; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 267 TGTCCAAAGGTTTATAGCAAGAGGTCGCAAAAGTGTATTTGCTGCTACAGAT 326
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QY 327 GCGTGGCGGCAACACCTTACTACATTAATAATCTGACGCGGCAATTAATTAATTA 386
|||
Db 375 AGATGACGTGAACACAGTTGATTTTAACTAACCAATGATATCTTATGAGACTGAAC 434
QY 387 CGT 389
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Db 435 AGT 437

RESULT 4
US-08-781-986A-4008
; Sequence 4008, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/781,986A
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

[illegible]

Db 305 ..DBCBHAB..MS.NSM.Y.BM.YM..Y.CH.B.RYNN.TS.NCA.D...AM.SR.W. 246

QY 435 TCCGGGACACAGATCCAAATCAAAAGATTTTATACACATCCATTCATTACAGCAGTCCGATAT 494

Db 245 ..M.HA.M.D.TY.N.Y..T.T.T..MTTADR.W..M.CA..T.S..ABH...M.B 186

QY 495 GATTGTCATGATTAATCTATTCATCAAAATTAGAGCGTGCTAAAAACGCTCAAAATTCATGGCGT 554

Db 185 ...B.H.BAH..CS.K..D...MH.TNMA.Y.Y.MH.AM.NN.N.Y..MN.SB.S..BT. 126

QY 555 TGGGACATTCGTTTATTGATGACACACCAAGTCAACAGCTGATTTAAAGAGACATCAA 614

Db 125 YMSR..HR.H..D.K.T.HNNBH..HRS.S..Y.S..SRMM.STY.KMW.ARKQ..CR.. 66

QY 615 CGCGCGGGGGCCCAA 628

Db 65 B.S..R.ST..M..A 52

RESULT 10

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US-10-184-634-412/c
: Sequence 412, Application US/10184634
: Publication No. US20030068684A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Chen, Jian
: APPLICANT: Desnoyers, Luc
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Pan, James
: APPLICANT: Smith, Victoria
: APPLICANT: Watanabe, Collin K.
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3430R1C217
: CURRENT APPLICATION NUMBER: US/10/184,634
: CURRENT FILING DATE: 2002-06-28
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 612
: SEQ ID NO 412
: LENGTH: 546
: TYPE: PRT
: ORGANISM: Homo Sapien
: US-10-184-634-412

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Best Local	7.0%	Pred.	No. 2.3				
Matches	26	Mismatches	252	Indels	0	Gaps	0

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          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      615 CGGCAGGGGGGCCAAA   628
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db       65 B.S.R.SP..M..A 52
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RESULT 11

US-09-917-800A-846/c
Sequence 846, Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 846
LENGTH: 597
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020119462A1 A11692339
US-09-917-800A-846

Query Match	5.28;	Score 33.2;	DB 10;	Length 597;
Best Local Similarly	56.48;	Pred. No. 3.7;		
Matches 62;	Conservative	0;	Mismatches 48;	Indels 0;
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QY	303	AGTGATATTGTGCTCACAGTATGGGTGGCGGAACACACCTTACTACA	352
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RESULT 12

Db 245 ..M.HA..M.D.TY..N.Y..T.T.T..MTTADR..W..M.CA..T.S...ABH....M.B 186
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 Db 185 ..B..H..BAH..CS..K..D...MH..TNMA..Y..MH..AW..NN..N..Y..MY..SB..S...BT. 126
 US-10-147-467-1
 : Sequence 1, Application US/10147467
 : Publication No US20030027295A1
 :
 : GENERAL INFORMATION:
 : APPLICANT: TAKESHI, Ishii
 : APPLICANT: SATOSHI, Mitsuda
 : TITLE OF INVENTION: ESTERASE GENE AND ITS USE

Mon May 19 10:47:08 2003

us-09-905-666a-1.rnpb

Page 7

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 Db 130 GAAGTGGTGAATCTTACATTGAAGTCGCCGAAATTCACGACAACTTGAATC 182

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Job time : 405 secs

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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2003, 05:34:24 ; Search time 1077 Seconds
(without alignments)
9609.021 Million cell updates/sec

Title: US-09-905-666a-1
Perfect score: 639
Sequence: 1 atgaattgttaaaagaag.....ggggccaaatacgaattaa 639

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	42.2	6.6	1101	17	CNS00L78
2	39	6.1	710	13	B1678753
3	37.8	5.9	628	17	AL760893
4	37	5.8	354	13	BG940033
5	37	5.8	646	17	AQ989712
6	37	5.8	704	14	BQ775177

Result No.	Score	Query Match %	Length	DB ID	Description
7	36.8	5.8	402	14	BQ253545
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9	36.8	5.8	444	12	BG043888
10	36.8	5.8	495	14	BQ741211
11	36.8	5.8	508	14	BQ079412
12	36.8	5.8	528	14	BM954819
13	36.8	5.8	539	14	BM954950
14	36.2	5.7	661	17	AQ991444
15	36.2	5.7	676	14	BQ458251
16	36	5.6	455	9	A1457833
17	36	5.6	629	17	A2356293
18	36	5.6	698	17	A2356093
19	35.4	5.5	386	10	AW544638
20	35.4	5.5	691	13	B1969075
21	35.2	5.5	707	17	BH607139
22	35.2	5.5	897	17	CNS005NL
23	35	5.5	808	17	CNS02659
24	35	5.5	1101	17	CNS0183L
25	34.8	5.4	664	17	A2522069
26	34.8	5.4	945	17	CNS0130R
27	34.6	5.4	408	10	AV536563
28	34.6	5.4	426	14	BM965989
29	34.6	5.4	548	14	BM965977
30	34.6	5.4	567	14	BQ089146
31	34.6	5.4	620	14	BQ458269
32	34.4	5.4	631	17	A2939720
33	34.4	5.4	827	17	BH671466
34	34.4	5.4	947	14	BQ719062
35	34.4	5.4	1101	17	CNS0160S
36	34.4	5.4	1101	17	CNS0181N
37	34.2	5.4	261	12	BG319118
38	34.2	5.4	344	14	BM815886
39	34.2	5.4	422	10	AV788662
40	34.2	5.4	1101	17	CNS012UB
41	34	5.3	900	13	BM468757
42	34	5.3	938	17	CNS006TJ
43	34	5.3	1304	10	BE531285
44	33.8	5.3	437	10	BE544807
45	33.8	5.3	438	12	BG045372

ALIGNMENTS

RESULT 1
LOCUS CNS00L78
DEFINITION Drosophila melanogaster genome survey sequence TEn3 end of BAC: BACR24B18 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL068157
VERSION AL068157.1 GI:4958085
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster.
KEYWORDS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
GENOSCOPE.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see: http://www.fruitfly.org/TheBDGP/Drosophila_melanogaster_BAC_library was prepared by Kazutoyo Osoegawa and Aaron Mamooser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial

EscoRII digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Source

BASE COUNT	294 a	182 g	307 t	106 others
ORIGIN				
	/organism="Drosophila melanogaster"			
	/db_xref="taxon:7227"			
	/clone_lib="BACR24B18"			
	/clone_lib="RPCT-98"			
	/note="end : TET3"			

Query Match	6.6%	Score 42.2	DB 17	Length 1101
Best Local Similarity	33.2%	Pred. No. 0.13		
Matches 76	Conservative 50	Mismatches 103	Indels 0	Gaps 0

OY 3 GAAATTTGTAAGGAAGGATCACTTGGCATTCACACTTTTGSTGTGCAGCACATC 62
 | | | | | | : | : | : | : | : |
Dd 799 GAATTATTTKAAAAAACYTCGACAMGCCVATTTGTTATAAATTTTTTKKKTTTTTTTTTTT 858

Qy 63 GCTGTTTGGCATGCACCCGTCAGCAAAAAGCCGCTGACACAAATCCAGTGTATTATGCTTCA 122

Db 859 TTTTATCTCMCGAAAAAAATWTTGMAAAAMMYTGKAWAMAAAMWTCACATTTKYVTTRSCAM 918

Oy 123 CGGTAATCGGAGGACCTTCATAAATTTTGGCGGAATTAAAGAGCATTCTCGATCTCA6GG 182

 :: : | :: | ||| : : : | | : : : | : | :

Db 919 TKGTTMCCCTARDTTSYATAAAATTTCTKRASATGGKCAAYTRRYSGGAAWTTCSKTG 978

Oy 183 CTGTCACGGGGCAAGCTGTATCGGGTGTATTTTTGGACAAGACAGGG 231
| | : : | : : : : : | : : : : :
Db 979 RAGGGRAAVSCTTTTKRRRARVGGCKCWTTKRGGSECKGTMVAGR 1027

RESULT 2
BI678753

DEFINITION	SWS601 SWS (Sapwood of black locust - Summer) <i>Robinia pseudoacacia</i>
CDNA, mRNA	sequence.
ACCESSION	BI678753

KEYWORDS	EST.
SOURCE	Robinia pseudoacacia.
ORGANISM	Robinia pseudoacacia

Robinia.

TITLE	AUTHORS	ABSTRACT
Analysis of gene expression patterns in trunk wood of a mature	Han, K.-H., Yang, J., Park, S., Paule, C.R., Kapur, V., Retzel, E.F., Kamdem, D.P. and Keathley, D.E.	

JOURNAL *Euterpe fuscata* (Nothofagaceae)
COMMENT Unpublished (2002)

Contact: Kyung-Hwan Han
Department of Forestry

Michigan State University
126 Natural Resources, East Lansing, MI 48824-1222, USA
Tel: 517 353 4751
Fax: 517 432 1143

FEATURES	Email: nanxy@msu.edu.
source	Location/Qualifiers
	1. .710
	/organism="Robinia

```

/clone_id="SMS (Sapwood of black locust - Summer)"
/tissue_type="sapwood"
/dev_stage="mature tree"
/notes="Vector: lambda Triplex; site_1: Sfi IA; site_2: Sfi
IB; The cDNA library was made from the sapwood of a mature

```

black locust tree collected in Michigan in late July.				
BASE COUNT	252 a	124 c	101 g	228 t
ORIGIN				5 others

Query Match	6.1%	Score 39;	DB 13;	Length 710;
Best Local Similarity	61.28;	Pred. No. 1;		
Matches 63;	Conservative	0;	Mismatches 40;	Indels 0;
			Gaps	0

Qy 418 ACGACAAAGCAAGGCCCTTCCGGGAMCAGATCCAAATCAAAAGATTTTATACACATCCATT 4777

Oy	478	TACAGCAGTGGCGATATGATTGTGCATGAATTACTTATCAAAAT	5200
Db	324	TAAAAAATGAAAAATTCAAATGACATTAAATTTAAAAATCAAAAT	3666

RESULT 3
AL760893/c

DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-203F11-014507,
genomic survey sequence.
ACCESSION AL760893

KEYWORDS	GSS.
SOURCE	thale cress.
ORGANISM	<i>Arabidopsis thaliana</i>

REFERENCE
1
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

TITLE A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from *Arabidopsis thaliana* T-DNA and Weisshaar, B.

JOURNAL	Unpublished
REFERENCE	2
AUTHORS	Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisschaar, B.

JOURNAL
REFERENCE
Unpublished
3 (bases 1 to 628)

TITLE Direct Submission
SUBMITTED (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germ

COMPLAINT
This sequence is retrieved from the EMBL database. It indicates an insertion close to or within gene Atg519740. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Katproject. GABI-Kat is part of the German

FRANK GENIUMICS PROGRAM DESIGNATED GABRIEL INFORMATION ON LINE
AVAILABILITY CAN BE FOUND AT:
<http://www.mpl2-koeln.mpg.de/GABI-Rat/>
LOCATION/QUALIFIERS

```
source
1. 020
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db xref="taxon:3702"
```

clone=6K-203F11-01450/
/clone_1b="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from

vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant

BASE COUNT	214 a	100 c	102 g	212 t
ORIGIN	processed for submission. T-DNA derived sequences were removed"			

Query Match	5.9%	Score 37.8;	DB 17;	Length 628;
Best Local Similarity	54.7%;	Pred. No. 2.2;		
Matches 75; Conservative	0;	Mismatches 62;	Indels 0;	Gaps 0;

throughput (NIH intramural sequencing center
http://www.nisc.nih.gov/)." 87 a 66 c 78 g 123 t

Qy	441	AAAGATCCAAATTAAGAAAGATTTATATACATTCATTTAAGACGCGCCATTAATGATT	500
Db	245	AAAAGATCAAACTCGTATGAGTAGTACCAAAATCTGTTGCTATATGAACCTTAACATTAAG	186
Qy	501	CATGAATTAACCTATATCAAAATTTAGACGCTGCTAAAAACGTCAAATTCATGCGCTGGGCA	566
Db	185	AAATGATTAATATGACCAAAATATGTAAGTAGATCAAAACAGCAAAAGCTTTTCCGTTAGTA	128
Qy	561	CATTGCTTAATATGATGA	577
Db	125	TTTTTCATTTTAAGATAA	109

Query Match	5.8%;	Score 37;	DB 13;	Length 354;
Best Local Similarity	50.3%;	Pred. NO. 3.2;		
Matches	91;	Conservative	0;	Mismatches 90;
			Indels	0;
			Gaps	0;

RESULT	
LOCUS	BG940033/C
DEFINITION	BC940033 354 bp mRNA linear EST 11-JUN-2001 ax03b04.f1 Proliferating Human Erythroid Cells (LDB:ax library)
ACCESSTION	Homo sapiens cDNA ax03b04 random, mRNA sequence. BC040022

[illegible]

ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 354)
Gubin,A.N., Njoroge,J.M., Bouffard,G.G. and Miller,J.L.
Gene expression in proliferating human erythroid cells
Genomics 59 (2), 168-177 (1999)
99339981
Contact: Jeffery L. Miller

RESULT 5
A0988712

National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda, MD

ONCHITIN
 PROTEOLYTIC ACTIVITY OF *Enterobacteriaceae*,
Photobacterium, *Proteobacteria*; gamma subdivision; *Enterobacteriaceae*,
Photobacterium.
 1 (bases 1 to 646)
 French-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
 AUTHORS

FEATURES

DNA Sequencing and analyses by National Institutes of Health Intramural Sequencing Center (NISC).
Plate: 03 row: b column: 04
Seq primer: -40M13 forward primer (Amersham).
Location/Qualifiers

JOURNAL MEDLINE COMMENT
Photorehabilitation of Mycobacterium tuberculosis
 Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
 20378633
 Contact: french-Constant RH
 Department of Biology and Biochemistry
 University of Bath
 South Building, Bath BA2 7AY, UK

Source

1.354

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ax03b04"
/clone_lib="Proliferating Human Erythroid Cells (LCB:ax03b04)"

```

```
/sex="unknown"
```

```
/cell_type="Erythroid cells"
```

Mononuclear Cells^a

```

/uev_scsge- plogentrol, EFO responsive CD/11ttt

```

```
/note="Organ: blood; Vector: Lambda 2AP II; Site_1: ECORI;
```

the buffy coat of a blood donation were obtained by flow

presence of erythropoietin. Total RNA was purified from

the source population using K1201 reagent. K1201 was converted into double-stranded cDNA using

Clontech's CapLibrary Construction Kit

cloned into EcoRI digested Lambda Zap II vector

to in vivo excision in SOLT.P cells. Individual colonies

were grown, and the DNA inserts were sequenced in 1991

FEATURES

Location/Qualifiers

Source

```

/organism="Photorhabdus luminescens"
/strain="W14"
/db_xref="taxon:29488"
/clone="PI600339"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"

```

```
/dev_stage="primary phase variant"
```

kb) and then cloned into M13 Janus."

E 08: 6000 37, DB 17, 100th 616

[illegible]

```

Query Match      5.8%; Score 37; DB 14; Length 704;
Best Local Similarity 50.3%; Pred. No. 4;
Matches          91; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY    450 AATCAACAAGATTGTTTGTACACATTCATTAAGCAGCGTGCCGATATGCATGAATAA 509
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     278 AAAATAAATAGAATTTTATATATATATGCTCATATATATATATATATATAAGATNAACGT 337

QY    510 CTATCAAATTAGACGGTGTAAAAACGCCAACATTTATGCGCGTGGCACATTGTTTT 569
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     338 TTCAACCATAATACAAAATGTCCAAMCATATACAAAANAATCCCACATATGCTACAGGAGCG 397

QY    570 ATGTGTGAACGCCAAGCAACAGCGCTGATTAAGAACAGACTGAACGGCGGGCCCCAAA 629
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     398 ATTTRAGCTGCTCCGAACCAAGAGGCTTATACAGGTCCTGACCTGGGGGGACACAG 457

QY    630 T 630
        |
Db     458 T 458

RESULT 7
BOSJ3545/c   402 bp mRNA linear EST 03-MAY-2002
LOCUS       B0253545
DEFINITION  Gm-cl052-4435 5', mRNA sequence.
ACCESSION   B0253545
VERSION     B0253545.1 GI:20449421
KEYWORDS    EST.
SOURCE      soybean.
ORGANISM    Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabiales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1.(bases 1 to 402)
AUTHORS     Shoemaker,R., Reim,P., Vodkin,L., Erpellding,J., Coryell,V., Khanaa,A.,
            Bolia,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Stepien,M., Theising,B., Allen.M., Bowers,Y., Person,B., Swaller,T., Gibbons.M., Pope,D., Harvey.N., Schurr,R., Rittler,E.,
            Kohn,S., Shin,T., Jackson.Y., Cardenas.M., McCann,R., Waterston.R. and Wilson.R.
TITLE       Public Soybean EST Project
JOURNAL     Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel.: 314 286 1800
            Fax: 314 286 1810
            Email: est@wustl.wustl.edu
            This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Hunttsville, AL 35801 For further information call: (800)-533-4363 or contact: cculresgen.com web site: www.resgen.com
            Seq primer: -40RP from GlDco High quality sequence stop: 370.

FEATURES             Location/Qualifiers
         source                1..402
         /organism="Glycine max"
         /db_xref="taxon:3847"
         /clone="SOYBEAN CLONE ID: Gm-cl052-4435"
         /clone_1fb="Gm-cl052"
         /tissue_type="whole seedlings of greenhouse grown plants"
         /dev_stage="1 week old"
         /lab_host="DH10B"
         /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The Harosoy NIL was constructed and seed was provided by Dr. J. Specht, University of Nebraska (Shoemaker and Specht, 1995). The cDNA library was constructed from mRNA isolated from whole seedlings of 1 week old greenhouse grown plants. Complementary DNA was

```


adapters were ligated to the blunt-ended cDNA fragments

these two time points. Complementary DNA was synthesized

from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by M. Bhattacharyya in the laboratory of Dr. Randy Shoemaker at Iowa State University."

BASE COUNT 144 a 137 c 105 g 117 t
ORIGIN

Query Match 5.8%; Score 36.8; DB 14; Length 503;
Best Local Similarity 69.4%; Pred. No. 4.1;

Matches 50; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

OY 2 TGAATTGTAAGAGAGATGATTCATGCTTGTACATTTGGTGCTGCATGCACAT 61
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 192 TGAATTGGAAGAGAGATTTTGTGCTTGTGGGATGTTGTTATGTCGCACAT 133
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 62 CGCTGTTGCCA 73
||| ||| ||| |||

Db 132 CGCAGTTGGGA 121
||| ||| ||| |||

RESULT 12
BM954819/c

LOCUS 528 bp mRNA linear EST 14-MAR-2002
DEFINITION sam73805.y1 Gm-c1069 glycine max cDNA clone SOYBEAN CLONE ID:

ACCESSION BM954819
VERSION BM954819.1 GI:19453409

KEYWORDS EST.

SOURCE soybean.

ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 528)

Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna

AUTHORS

, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,

Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers

, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harney, N., Schurk

, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann

, R., Waterston, R. and Wilson, R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: Resgen, Invitrogen Corp. 2130

South Memorial Parkway Huntsville, AL 35801 For further information

call: (800)-533-4363 or contact: ccutresgen.com web site:

seedlings for the cultivar Williams. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

BASE COUNT 146 a 143 c 120 g 119 t
ORIGIN

Query Match 5.8%; Score 36.8; DB 14; Length 528;
Best Local Similarity 69.4%; Pred. No. 4.2;

Matches 50; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

OY 2 TGAATTGTAAGAGAGATGATTCATGCTTGTACATTTGGTGCTGCATGCACAT 61
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 188 TGAATTGGAAGAGAGATTTTGTGCTTGTGGGATGTTGTTATGTCGCACAT 129
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 62 CGCTGTTGCCA 73
||| ||| ||| |||

Db 128 CGCAGTTGGGA 117
||| ||| ||| |||

RESULT 13
BM954950/c

LOCUS 539 bp. mRNA linear EST 14-MAR-2002
DEFINITION sam75c01.y1 Gm-c1069 glycine max cDNA clone SOYBEAN CLONE ID:

ACCESSION BM954950
VERSION BM954950.1 GI:19453540

KEYWORDS EST.

SOURCE soybean.

ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 539)

Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna

AUTHORS

, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,

Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers

, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harney, N., Schurk

, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann

, R., Waterston, R. and Wilson, R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: Resgen, Invitrogen Corp. 2130

South Memorial Parkway Huntsville, AL 35801 For further information

call: (800)-533-4363 or contact: ccutresgen.com web site:

FEATURES

SOURCE

1. 528

/organism="Glycine max"

/db_xref="taxon:3847"

/clone="SOYBEAN CLONE ID: Gm-c1069-5289"

/tissue_type="Degenerating cotyledons, 9-10 day old

etiolated seedling"

/lab_host="DH10B"

FEATURES

SOURCE

1. 539

/organism="Glycine max"

/db_xref="taxon:3847"

/clone="SOYBEAN CLONE ID: Gm-c1069-5113"

/tissue_type="Degenerating cotyledons, 9-10 day old

etiolated seedling"

/lab_host="DH10B"

High quality sequence stop: 424.

Location/Qualifiers

1. 528

/organism="Glycine max"

/db_xref="taxon:3847"

/clone="SOYBEAN CLONE ID: Gm-c1069-5289"

/tissue_type="Degenerating cotyledons, 9-10 day old

etiolated seedling"

/lab_host="DH10B"

High quality sequence stop: 422.

Location/Qualifiers

1. 539

/organism="Glycine max"

/db_xref="taxon:3847"

/clone="SOYBEAN CLONE ID: Gm-c1069-5113"

/tissue_type="Degenerating cotyledons, 9-10 day old

etiolated seedling"

/lab_host="DH10B"

Mon May 19 10:47:09 2003

us-09-905-666a-1.rst

Page 9

QY 99 ACACATCCCACTTGTATATGGTTCACGGTATCGAGAGCTTCATACAAATTTGCGGGAT 158
 Db 172 AAAGCGCCCACTAGTGTTTTGTGCATGGTGTTCACAGCAGCCAGCAATGTTTGGTTAAGCA 231
 QY 159 TAAAGAGCTATCTCGTATCTCAGGCGCTGTACAGGCGCAACCTGATCGGTTATATTTTG 218
 Db 232 TCGTGAATATTTTCATCAACATGGCTATTCGCCAGCCGAGCTTTAGCCGACGACATATGG 251
 QY 219 GGACAAAGCAGGGGCGAATTTATACATTTGGCCCGGTATTTCACGATTTTGTCAAAAGT 278
 Db 292 TGACGGGGGGCTCCACAGAGCGATTTCGATGACCGAATCTTATGCAAGATTTTTCACAGAT 351
 QY 279 TTATAGCAAAACGGGTGCGAAAAAGAGATATTTGTGCTCACAGTATTTGGGTG 331
 Db 352 TCGTCAGCTAATATTCGCTGACAGAGTATACGGGAAGCAAAATTTGGATG 404

Search completed: May 18, 2003, 07:47:57
Job time : 1086 secs

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